

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 07-24-02
Searcher: Beverly 24994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 25
Number of Searches: _____
Number of Databases: 1

Search Site

____ STIC
____ CM-1
____ Pre-S

Type of Search

____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors

____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other CGN

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 13:10:30 / Search time 2538.62 Seconds

(Without alignments)
1642.845 Million cell updates/sec

Title: US-09-738-599-22

Perfect score: 309
Sequence: 1 atgcagataaataagatga.....gggtatattgcacacatag 309

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

EST:
1: em_estha:
2: em_esthum:
3: em_estin:
4: em_estnu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_estt:
9: gb_estl:
10: gb_est2:
11: gb_hic:
12: gb_gss:
13: em_gss_hum:
14: em_gss_inv:
15: em_gss_pin:
16: em_gss_vrt:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	228.6	74.0	332	9	AM619529 7594 MARC
C 2	183.8	59.5	731	9	AV398499 AV398499
C 3	140.4	45.4	240	9	AM659631 97104 MAR
C 4	139.8	45.2	785	9	AI547008 P42.1.13
C 5	123.8	40.1	223	10	C22108
C 6	117.2	37.9	160	10	BG895793 359430 MA
C 7	115.6	37.4	160	10	BG835172 353618 MA
C 8	109.4	35.4	336	10	BE521841 M22A1STM
C 9	106.2	34.4	162	10	BI338974 363710 MA
C 10	88.4	28.6	178	10	BI432815 EST55576
C 11	65.8	21.3	802	9	AI546999 P42.1.12
C 12	59.8	19.4	594	10	BE493915 WHE1276_B
C 13	45.2	14.6	560	12	B84811 RPT11.128F
C 14	45.2	14.6	634	12	AO309897 CITR1-EI
C 15	42.8	13.9	532	12	AO544521 CITR1-EI
C 16	42	13.6	299	9	AA547917 MB3D6260
C 17	38.8	12.6	914	12	AZ539756 ENTG955TR

C 18	38.6	12.5	426	9	AV532310	AV532310
C 19	38.6	12.5	599	9	AV537481	AV537481
C 20	38.4	12.4	520	12	AZ927608	AZ927608
C 21	38	12.3	514	12	BM168198	BM168198
C 22	37.4	12.1	183	12	B88032	B88032
C 23	37.4	12.1	544	12	AZ525395	AZ525395
C 24	37.2	12.0	488	12	AG024048	Oryza sat
C 25	37.2	12.0	942	12	CNS02FIE	AL194459 Tetradon
C 26	37	12.0	404	10	BI514353	BI514353
C 27	37	12.0	458	10	BI510802	BI510802
C 28	37	12.0	559	10	BI510865	BI510865
C 29	36.8	11.9	478	9	AM288591	AM288591
C 30	36.8	11.9	582	12	AQ029690	AQ029690
C 31	36.8	11.9	646	12	AZ522631	RPCI-11-4
C 32	36.8	11.9	681	10	BE658070	BE658070
C 33	36.4	11.8	733	10	BF680474	BF680474
C 34	36.2	11.7	500	9	AU086381	AU086381
C 35	36	11.7	617	12	AZ856405	AZ856405
C 36	36	11.7	713	12	BH029375	BH029375
C 37	36	11.7	1101	12	CNS01610	AL106770 Drosophila
C 38	35.8	11.6	494	10	BI745078	BI745078
C 39	35.8	11.6	496	9	AA842275	AA842275
C 40	35.6	11.5	885	12	CNS013ET	AL102767 Drosophila
C 41	35.4	11.5	771	9	AL516158	AL516158
C 42	35.4	11.5	1101	12	CNS058M7	AL350728 Tetradon
C 43	35.2	11.4	392	10	BM258478	BM258478
C 44	35.2	11.4	468	9	AV618307	AV618307
C 45	35.2	11.4	581	9	AM573687	AM573687

ALIGNMENTS

RESULT 1
LOCUS AM619529/c
DEFINITION 7594 MARC PBE Sus scrofa CDNA 5', mRNA sequence.
ACCESSION AM619529
VERSION AM619529.1 GI:7325713
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM Sus scrofa
Pig.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 332)
Smith,T.P.L., Fahrenkrug,S.C., Rohrer,G.A., Simmen,F.A., Rexroad
C.E. and Keefe,J.W.
Mapping of expressed sequence tags from a porcine early embryonic
CDNA library
Anim. Genet. 32 (2), 66-72 (2001).
21314990
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases cycled and alt. trimmed with phred
v0.960904.e. Vector identified by cross_match with the -minscore 18
and -match 12 options.
PCR Primers
FORWARD: GGAAACGATGACCATG
REVERSE: GTAAACGACGACCATG
Seq primer: AATTACCCCTAATAAGG.
Location/Qualifiers
1..332
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC PBE"
/issue_type="day 12 whole embryos"
/lab_host="XOLR"
/note="Vector: pBLUESCRIPT SK-; Site_1: EcoRI; Site_2:
XhoI; Library made from pool of embryos in spherical and

FEATURES
Source

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/organism="Bombyx mori"
/db_xref="taxon:7091"
/clone="NY021882"
/clone_id="Bombyx mori ovary BmNPV infected; 2 hr after
inoculation"
/tissue_type="ovary"
/cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 2 hr after inoculation"
BASE COUNT      194 a      171 c      164 g      202 t
ORIGIN

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Query Match	45.48; Score 140.4; DB 9; Length 240;
Best Local Similarity	90.48; Pred. No. 3.2e-28;

Db 75 TTTTGGGGGGGAGAAATGTTTAAACAGAAACCGAACAATCCTAANAGAT 16
105 CCGCGCGCGCGAGAGAAACGCGCAGAAACGAGAAACCGAACAATCCTAANAGAT 244

DEFINITION	3559430 MARC IP16
ACCESSION	BG895793
VERSION	BG895793.1 GI:14

old cDNA 5' , mRNA sequence.

SOURCE pig.
ORGANISM Sus scrofa
COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 160)
AUTHORS Fahrnering, S.C., Frickling, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.M., and Keeler, J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TP
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTACGACG
Plate: 123 row: L column: 23
Seq primer: ATTAGTGACATATAG.
Location/Qualifiers
1. 160
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_11b="MARC 1Pig"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPOR6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
BASE COUNT 46 a 37 c 31 g 46 t
ORIGIN
Query Match 37.9%; Score 117.2; DB 10; Length 160;
Best Local Similarity 93.8%; Pred No. 7.1e-22;
Matches 122; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 179 ccaaaattgttgcgtgagaaatgttgaacacagaactcagcaaatcgttaa 238
DB 160 CCAAAATTGTGCGGCGGCGAGAAATGTGTTAAACAGAAACCCGCAACATTCGTAA 101
QY 239 atgattgtcgtgtttatcactcttggcatctatactccgtggaagccgggtatatt 298
DB 100 ATGATTGTGCTCGGTTTATTACTTTAGGCACTTATACCTCGCTGGAAGCGGTGTATT 41
QY 299 gctcacaata 308
DB 40 GCTCACAAATA 31
RESULT 7
BG835172/c 160 bp mRNA linear EST 25-MAY-2001
LOCUS BG835172
DEFINITION 353618 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BG835172
VERSION BG835172.1 GI:14201080
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE -1 (bases 1 to 160)
AUTHORS Fahrnering, S.C., Frickling, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.M., and Keeler, J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine

JOURNAL Unpublished (2000)
COMMENT Contact: Smith TP
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTACGACG
Plate: 116 row: L column: 23
Seq primer: ATTAGTGACATATAG.
Location/Qualifiers
1. 160
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_11b="MARC 1Pig"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPOR6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
BASE COUNT 47 a 37 c 31 g 45 t
ORIGIN
Query Match 37.4%; Score 115.6; DB 10; Length 160;
Best Local Similarity 93.1%; Pred. No. 1.9e-21;
Matches 121; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 179 ccaaaattgttgcgtgagaaatgttgaacacagaactcagcaaatcgttaa 238
DB 160 CCAAAATTGTGCGGCGGCGAGAAATGTGTTAAACAGAAACCCGCAACATTCGTAA 101
QY 239 atgattgtcgtgtttatcactcttggcatctatactccgtggaagccgggtatatt 298
DB 100 ATGATTGTGCTCGGTTTATTACTTTAGGCACTTATACCTCGCTGGAAGCGGTGTATT 41
QY 299 gctcacaata 308
DB 40 GCTCACAAATA 31
RESULT 8
BE521841 336 bp mRNA linear EST 19-MAR-2001
LOCUS BE521841
DEFINITION M22A1STM Arabidopsis developing seed Arabidopsis thaliana cDNA
ACCESSION BE521841
VERSION BE521841.1 GI:9779819
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
COMMENT Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotys; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 336)
AUTHORS White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ibarra, O., Jaworski, J.G., Ohlrogge, J., and Banning, C.
TITLE A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil
JOURNAL Plant Physiol. 124 (4), 1582-1594 (2000)
COMMENT Contact: Banning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
USA
Tel: 517 355 1609
Fax: 517 353 9334

VERSION	B84811.1	GI:2925943
KEYWORDS	GSS.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 560)	
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.Golden,K., Berry,R., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.	
TITLE	Use of BAC End Sequences for Sequence-Ready Map Building (1998)	
JOURNAL	Unpublished (1998)	
COMMENT	Other-GSS: RPC11-2857.TV Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Plietser de Jong (plieter@jong.med.buffalo.edu). Clones may be purchased from BACPac Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tcb/humgen/bac_end_search/bac_end_search.html Seq primer: GSP6 Class: BAC ends.	

FEATURES	SOURCE	Location/Qualifiers
	1. 560	/organism="Homo sapiens"
		/db_xref="GDB:7510494"
		/db_xref="taxon:9606"
		/clone_11b="RPC1-11-28F"
		/clone_11b="RPC1-11"
		/sex="Male"
		/cell_type="lymphocytes"
		/notes="Vector: pBAC3.6; Site.1: EcoRI; Site.2: EcoRI; RpsIII Human Male BAC library"
BASE COUNT	240 a	106 c 82 g 132 t
ORIGIN		

Query Match	14.6%	Score 45.2;	DB 12;	Length 560;
Best Local Similarity	48.8%;	Pred. No. 0.04%;		
Matches 122;	Conservative 0;	Mismatches 128;	Indels 0;	Gaps 0
QY 8	ataataagatgtaaaaaaatgttattctctgcgcgtctgccaatgcttataacagatgtg 67			
Db 269	ATTGAAACAAAGCAAGATGCTTACTTTGGCTACTCCATCCACACTTAATCTAGAAAGTG 328			
QY 68	ctcaacaacgcttactctgttgaaacaacaacgcaacgacgtacacccaagaagaacatca 127			
Db 329	CTAGCCAAACAACTAGGTAAAGTAAATCAAAAGGCGCTCAAAACAAAAAGAAAGTAAAA 388			
QY 128	ctcacatctctctcgttcgcggaattggacaagaagaacatcgttgatgcagccaaattc 187			
Db 389	TATCTCTCATCTAGGATTATATAAATTCTATACTAGAGAACCCCTGGAGACCAACCAAGA 448			
QY 188	gtgcgcgtgcagaagaatcgtttaaacaagaacactcgcgaacatcgttaatygatctgc 247			
Db 449	CTCCGGCTACGATATATCTCAGTAAAGTTTCAGAGTACAAATTAAGTGACAAAAAATTAG 508			
QY 248	tcggtttat 257			
Db 509	TAGCATTTT 518			

LOCUS	DEFINITION	LOCUS	DEFINITION
AO309897	AO309897	634 bp	DNA
CTBT-E1-2522C23	CTBT-E1-2522C23	1 linear	GSS 22-DEC-1997
DNA sequence.	DNA sequence.		genomic clone 2522C23,

ACCESSION	AO309897	
VERSION	AO309897.1	GI:4041764
KEYWORDS	GSS.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Adamakytova; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (Passes 1 to 634)	
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., and Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,D.C.	
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building	
JOURNAL	Unpublished (1998)	
COMMENT	Other_GSSS: CITBI-El-2522C23.TF Contact: Shaying zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbeetlgr.org Clones are available from Research Genetics (Info@resgen.com). BAC end search page: http://www.tlgr.org/tlgr/hungen/bac_end_search/bac_end_search.html Seq primer: M13 Reverse Class: BAC ends.	

FEATURES	source	Location/Qualifiers
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	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="252C23"	
	/clone_11p="CITB1-E1"	
	/sex="male"	
	/cell_type="sperm"	
	/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI"	
BASE COUNT	274 a	123 c 89 g 148 t
ORIGIN		

	Query Match	14.6%	Score 45.2;	DB 12;	Length 634;	
	Best Local Similarity	48.8%;	Pred. No. 0.05;			
	Matches 122;	Conservative	0;	Mismatches 128;	Indels	Gaps
Oy	8 ataataagatgaanaaaattgttattttctgcgcgctcgcaattggtattacaggatg	67				
Db	309 ATTGAATCAAGCAAGGATGCTTACTTTGTCTACTCCCATCCAACTAATACTTAGAAGTG	368				
Oy	68 ctcaacaacagtcttcgtcttgaaaacaaccagcacagtaaccaaacagaacatca	127				
Db	369 CTAGCCAACACATCAGTAAAGTAAATCAAAAGCGCTCAAACAAAAGAACGCATAAA	428				
Oy	128 ctcatcatttcttcglttcggaaattggaacagaagaactgtgtacgccaattt	187				
Db	429 TATCTTCATCATGTATTATAAAATTCTAATCTAGAGAACCCTGGAGAACCAACAAGA	488				
Oy	188 gtgcgcgtgcagaaaaatgttgttaaacaagaacctcagcaaacattcgtaaatgattgc	247				
Db	489 CTCCTGGTACTGATTAATCTCAAGTAAGTTTCAGGTACAAATAATAGTGACAAAAATTAG	548				
Oy	248 tccgatttat 257					
Db	549 TAGCATTTTT 558					

RESULT	15
AO544521	
LOCUS	532 bp DNA linear GSS-28-MAY-1996
DEFINITION	CITR1-EI-2636G14.TR CITR1-EI Homo sapiens genomic clone 2636G14,
ACCESSION	DNA sequence.
VERSION	AO544521.1 GI:4904043

GenCore version 4.5
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OM nucleole - nucleole search, using sw model

Run on: July 23, 2002, 13:45:07 ; Search time 99.46 Seconds
(without alignments)
763.128 Million cell updates/sec

Title: US-09-738-599-22

Perfect score: 309
Sequence: 1 atgcagagataataagatgaa.....gggtatattgctcacaatag 309

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database: Issued_Patents_NA:*
1: /cgn2_6/prodata/2/lna/5A.COMB.seq:*
2: /cgn2_6/prodata/2/lna/5B.COMB.seq:*
3: /cgn2_6/prodata/2/lna/5A.COMB.seq:*
4: /cgn2_6/prodata/2/lna/5B.COMB.seq:*
5: /cgn2_6/prodata/2/lna/PCTUS.COMB.seq:*
6: /cgn2_6/prodata/2/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	309	100.0	309	3	US-09-023-221A-22
2	309	100.0	309	4	US-09-282-352A-22
3	309	100.0	378	3	US-09-023-221A-21
4	309	100.0	378	4	US-09-282-352A-21
5	309	100.0	760	3	US-09-023-221A-1
6	309	100.0	760	4	US-09-282-352A-1
7	273.2	88.4	309	3	US-09-023-221A-5
8	273.2	88.4	309	4	US-09-282-352A-5
9	252	81.6	309	3	US-09-023-221A-6
10	252	81.6	309	4	US-09-282-352A-6
11	252	81.6	11933	4	US-09-470-618-13
12	252	81.6	11933	4	US-09-364-862-13
13	34.2	11.1	1519	4	US-09-002-361-4
14	33.6	10.9	1817	2	US-08-743-637B-1
15	33.6	10.9	1817	3	US-08-526-840B-1
16	32.8	10.6	4380	1	US-07-582-941-1
17	32.8	10.6	4380	2	US-08-453-141-1
18	32.8	10.6	4380	3	US-08-453-141-1
19	32.4	10.5	1925	3	US-08-293-314-1
20	32.2	10.4	408	4	US-09-328-111-169
21	32.2	10.4	1690	1	US-08-276-452A-24
22	32.2	10.4	1690	2	US-08-798-744-24
23	31.2	10.1	90050	4	US-09-245-041-5
24	30.6	9.9	1504	4	US-08-878-989-10
25	30.6	9.9	1504	2	US-09-372-796-10
26	30.6	9.8	1576	4	US-09-197-378-1
27	30.2	9.8	2089	1	US-08-552-142A-1

C 28	30.2	9.8	2089	1	US-08-910-973-1	Sequence 1, Appl1
C 29	30.2	9.8	2089	5	PCT-US95-05741-1	Sequence 1, Appl1
C 30	29.8	9.6	2431	3	US-08-714-918-15	Sequence 15, Appl1
C 31	29.8	9.6	2431	4	US-09-265-315-15	Sequence 15, Appl1
C 32	29.8	9.6	2431	4	US-09-265-315-15	Sequence 15, Appl1
C 33	29.8	9.6	2431	4	US-09-266-417-15	Sequence 15, Appl1
C 34	29.8	9.6	2431	2	US-08-788-892-1	Sequence 1, Appl1
C 35	29.6	9.6	2525	3	US-08-714-918-84	Sequence 84, Appl1
C 36	29.6	9.6	2525	4	US-09-265-315-84	Sequence 84, Appl1
C 37	29.6	9.6	2525	4	US-09-265-315-84	Sequence 84, Appl1
C 38	29.6	9.6	3825	3	US-08-266-417-84	Sequence 84, Appl1
C 39	29.6	9.6	3825	3	US-08-904-263A-3	Sequence 3, Appl1
C 40	29.4	9.5	237	3	US-08-904-263A-3	Sequence 3, Appl1
C 41	29.4	9.5	846	2	US-08-743-637B-189	Sequence 189, Appl1
C 42	29.2	9.4	595	4	US-09-385-982-25	Sequence 25, Appl1
C 43	28.8	9.3	906	2	US-08-951-871-5	Sequence 5, Appl1
C 44	28.8	9.3	4248	3	US-08-678-614-1	Sequence 1, Appl1
C 45	28.6	9.3	3414	1	US-07-973-320-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-023-221A-22
Sequence 22, Application US/09023221A
Patent No. 6087128
GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255,00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-023-221A-22

Query Match 100.0%; Score 309; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.4e-86;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 atgcagagataataagatgaaatgttttttcgcgctgtggaatgctattaca 60
|||||
atgcagagataataagatgaaatgttttttttcgcgctgtggaatgctattaca 60

Query Match	100.0%;	Score 309;	DB 4;	Length 309;
Best Local Similarity	100.0%;	Pred. NO. 5.4e-86;		
Matches 309;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	atgcagataataaagatgaaaaaatgtattttctgcgcctctggcaatgcttata	60	

Query_Match	100.0%	Score 309;	DB 3	Length 378;
Best Local Similarity	100.0%	Pred. No. 5.8e-86;		
Matches 309;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Q7	1	atgcgcgataataaagatgaaaaaatgtattttctgcgcgtctgcgaatgcttattaca	60	
Db	34	ATGCGGATAAATAAATGTAATTTCTGCCGCGCTGGCAATGCTATTATACA	93	

QY 61 ggaatgctcaacaacgcttactgttggaaacaacacgagcagtaacacccaagaa 120
DB 94 GGATGTCCTCAACAAAGCTTACTGTTGGAAACAAACCGACAGTAACACCAAGAA 153
QY 121 accatacctcaatcattcttcgttgcgggaattggacaagaanaactgtatgcagcc 180
DB 154 ACCATACATCATATTTCTTCGTTGGGAATTGACAAAGAAACTGTTGATGCAGCC 213
QY 181 aaatttggcggcggtcagaaatgttgttaaacagaaactcagcaaacattcgtaaat 240
DB 214 AAAATTGTCGCGGTGACAGAAATGTTTAAACAGAAACTCAGCAACATTGCTAAAT 273
QY 241 ggaatcctcggttttactcatttggacatcatactccgctggagccgggtatattgc 300
DB 274 GGATGTCGCGGTGTTTACATTTTGGCATCTATACCTCGGTGGAAGCCGGGTATATTGC 333
QY 301 tcacaatag 309
DB 334 TCACAAATAG 342

RESULT 4

US-09-282-352A-21

Sequence 21, Application US/09282352A

Patent No. 6187321

GENERAL INFORMATION:

APPLICANT: NOLAN, LISA K.

APPLICANT: HORNE, SHELLEY M.

APPLICANT: ROBINSON, MICHAEL

TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEETING, RAASCH & GERHARDT P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: U.S.A.

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/282,352A

FILING DATE: 31-MAR-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/023,221

FILING DATE: 12-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG MS., VICTORIA A.

REGISTRATION NUMBER: 41,287

REFERENCE/DOCKET NUMBER: 255,00010102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 305-1226

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 378 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-282-352A-21

DB 34 ATCCAGATATATATGAAATTAATTTCTGCGCGCTCTGCAATGCTTATTACA 93
QY 61 ggaatgctcaacaacgcttactgttggaaacaacacgagcagtaacacccaagaa 120
DB 94 GGATGTCCTCAACAAAGCTTACTGTTGGAAACAAACCGACAGTAACACCAAGAA 153
QY 121 accatacctcaatcattcttcgttgcgggaattggacaagaanaactgtatgcagcc 180
DB 154 ACCATACATCATATTTCTTCGTTGGGAATTGACAAAGAAACTGTTGATGCAGCC 213
QY 181 aaatttggcggcggtcagaaatgttgttaaacagaaactcagcaaacattcgtaaat 240
DB 214 AAAATTGTCGCGGTGACAGAAATGTTTAAACAGAAACTCAGCAACATTGCTAAAT 273
QY 241 ggaatcctcggttttactcatttggacatcatactccgctggagccgggtatattgc 300
DB 274 GGATGTCGCGGTGTTTACATTTTGGCATCTATACCTCGGTGGAAGCCGGGTATATTGC 333
QY 301 tcacaatag 309
DB 334 TCACAAATAG 342

RESULT 5

US-09-023-221A-1

Sequence 1, Application US/09023221A

Patent No. 6087128

GENERAL INFORMATION:

APPLICANT: NOLAN, LISA K.

APPLICANT: HORNE, SHELLEY M.

TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEETING, RAASCH & GERHARDT P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: U.S.A.

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,221A

FILING DATE: 12-FEB-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG MS., VICTORIA A.

REGISTRATION NUMBER: 41,287

REFERENCE/DOCKET NUMBER: 255,00010101

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 305-1226

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 760 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-023-221A-1

Query Match 100.0%; Score 309; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 5.8e-86;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atcagagataataagatgaaanaaatgttattcttcgcgctctggcaatgcttattaca 60
DB 292 ATCGAGATATATATGAAATTAATTTCTGCGCGCTCTGCAATGCTTATTACA 351

Query Match 100.0%; Score 309; DB 3; Length 760;
Best Local Similarity 100.0%; Pred. No. 7.6e-86;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atcagagataataagatgaaanaaatgttattcttcgcgctctggcaatgcttattaca 60
DB 292 ATCGAGATATATATGAAATTAATTTCTGCGCGCTCTGCAATGCTTATTACA 351

QY 61 ggaatgctcaacaacagcttactgttggaacaacacagcagcagtaacacaaagaa 120
 Db 352 GGATGCTCAACAAGAGTTACTGTGGAAACAAACGACAGATACACCAAGAA 411
 QY 121 accatcaatcatcttcttcgttcggaattgacaagaagaactgttgatgcagcc 180
 Db 412 ACCATCACTCATCTTCTTCTGTTCCGGAAATTGGACAGAGAAAGCTGTGATGCAACC 471
 QY 181 aaattgtgagcggtgcagaaatgtgttaaaacagaaactcagcaacattcgttaat 240
 Db 472 AAAATTGTGGCGGTGCAGAAATGTGTAAACAGAAACTCAGCAAACTGTGTAAT 531
 QY 241 ggaatgctcggtttatcaacttttgcatctatctcgcgtggaagccggtatattgc 300
 Db 532 GGATGCTCGGTTTATCACTTTGGCATCTATCTCCGCGAAGCCCGGGTATATTGC 591
 QY 301 tcacaatag 309
 Db 592 TCACAATAG 600

RESULT 6
 US-09-282-352A-1
 ; Sequence 1, Application US/09282352A
 ; Patent No. 6187321

; GENERAL INFORMATION:
 ; APPLICANT: NOLAN, LISA K.
 ; APPLICANT: HORNE, SHELLEY M.
 ; APPLICANT: ROBINSON, MICHAEL
 ; TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MOETING, RAASCH & GEBHARDT P.A.
 ; STREET: 119 NORTH FOURTH STREET, SUITE 203
 ; CITY: MINNEAPOLIS
 ; STATE: MN
 ; COUNTRY: U.S.A.
 ; ZIP: 55401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/282,352A
 ; FILING DATE: 31-MAR-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/023,221
 ; FILING DATE: 12-FEB-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SANDBERG MS., VICTORIA A.
 ; REGISTRATION NUMBER: 41,287
 ; REFERENCE/DOCKET NUMBER: 255,00010102
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (612) 305-1226
 ; TELEFAX: (612) 305-1228
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 760 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-09-282-352A-1

Query Match 100.0%; Score 309; DB 4; Length 760;
 Best Local Similarity 100.0%; Pred. No. 7.6e-86;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 atcagagataataagaataaataatgtttctgcgcgtctggaatgctattaca 60
 Db 1 atcagagataataagaataaataatgtttctgcgcgtctggaatgctattaca 60

Db 292 ATGAGATATATAGATGAAAAATGTTATTCTGCGCTCTGCGCAATGCTTATTACA 351
 QY 61 ggaatgctcaacaacagcttactgttggaacaacacagcagcagtaacacaaagaa 120
 Db 352 GGATGCTCAACAAGAGTTACTGTGGAAACAAACGACAGATACACCAAGAA 411
 QY 121 accatcaatcatcttcttcgttcggaattgacaagaagaactgttgatgcagcc 180
 Db 412 ACCATCACTCATCTTCTTCTGTTCCGGAAATTGGACAGAGAAAGCTGTGATGCAACC 471
 QY 181 aaattgtgagcggtgcagaaatgtgttaaaacagaaactcagcaacattcgttaat 240
 Db 472 AAAATTGTGGCGGTGCAGAAATGTGTAAACAGAAACTCAGCAAACTGTGTAAT 531
 QY 241 ggaatgctcggtttatcaacttttgcatctatctcgcgtggaagccggtatattgc 300
 Db 532 GGATGCTCGGTTTATCACTTTGGCATCTATCTCCGCGAAGCCCGGGTATATTGC 591
 QY 301 tcacaatag 309
 Db 592 TCACAATAG 600

RESULT 7
 US-09-023-221A-5
 ; Sequence 5, Application US/09023221A
 ; Patent No. 6087128

; GENERAL INFORMATION:
 ; APPLICANT: NOLAN, LISA K.
 ; APPLICANT: HORNE, SHELLEY M.
 ; TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MOETING, RAASCH & GEBHARDT P.A.
 ; STREET: 119 NORTH FOURTH STREET, SUITE 203
 ; CITY: MINNEAPOLIS
 ; STATE: MN
 ; COUNTRY: U.S.A.
 ; ZIP: 55401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,221A
 ; FILING DATE: 12-FEB-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SANDBERG MS., VICTORIA A.
 ; REGISTRATION NUMBER: 41,287
 ; REFERENCE/DOCKET NUMBER: 255,00010101
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (612) 305-1226
 ; TELEFAX: (612) 305-1228
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 309 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-023-221A-5

Query Match 88.4%; Score 273.2; DB 3; Length 309;
 Best Local Similarity 96.8%; Pred. No. 3.2e-75;
 Matches 309; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
 QY 1 atcagagataataagaataaataatgtttctgcgcgtctggaatgctattaca 60
 Db 1 atcagagataataagaataaataatgtttctgcgcgtctggaatgctattaca 60

QY 61 ggaatgctcaacaacgcttactgttggaaacaacagcagtaaacacaaagaa 120
DB 61 GGATGCTCAACAACGTTACTGTGGAAACAACCGACAGTAACCAAGGAA 120
QY 121 accatcaatcaatcttcttcgttcggaattggacaagaagaactgttgacgac 180
DB 121 ACCATCAATCATATCTTCTTCGTTCCCAATTGGAC-AGAGAAACTGTGATGACGCC 179
QY 181 aaatttg-tggcgtgacgaagaatgtgttaaacagaacacgaacattcgtaa 239
DB 180 AAAATTGTTGGCGGTGACGAAATGTTGTTAAACAGAACTCAGCAAACTTCGTA 239
QY 240 tggattgcgtgtttatcaacttttgacatctactcgtggaagccgggtatattg 299
DB 240 TGCATTGCCGGGTTTATCATCTTTGGCATCTATCTCCGGGGAACCCGTTATATTG 299
QY 300 ctcaaatag 309
DB 300 CTCACAATAG 309

RESULT 8

US-09-282-352A-5

Sequence 5, Application US/09282352A

Patent No. 6187321

GENERAL INFORMATION:

APPLICANT: NOLAN, LISA K.

APPLICANT: HORNE, SHELLEY M.

APPLICANT: ROBINSON, MICHAEL

TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MUEITING, RAASCH & GEBHARDT P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: U.S.A.

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/282,352A

FILING DATE: 31-MAR-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/023,221

FILING DATE: 12-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG MS., VICTORIA A.

REGISTRATION NUMBER: 41,287

REFERENCE/DOCKET NUMBER: 255.00010102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 305-1226

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-282-352A-5

Query Match 88.4%; Score 273.2; DB 4; Length 309;
Best Local Similarity 96.8%; Pred. No. 5.2e-75;
Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
QY 1 atcagagataataagatgaaaaaagtatttttcgcgcgtcttgcaagcttattaca 60
DB 1 atcagagataataagatgaaaaaagtatttttcgcgcgtcttgcaagcttattaca 60

DB 1 ATCAGAGATATAAGATGAAAAAATGTTATTTTCGCCCTCTGGCATGCTTATTACA 60
QY 61 ggaatgctcaacaacgcttactgttggaaacaacagcagtaaacacaaagaa 120
DB 61 GGATGCTCAACAACGTTACTGTGGAAACAACCGACAGTAACCAAGGAA 120
QY 121 accatcaatcaatcttcttcgttcggaattggacaagaagaactgttgacgac 180
DB 121 ACCATCAATCATATCTTCTTCGTTCCCAATTGGAC-AGAGAAACTGTGATGACGCC 179
QY 181 aaatttg-tggcgtgacgaagaatgtgttaaacagaacacgaacattcgtaa 239
DB 180 AAAATTGTTGGCGGTGACGAAATGTTGTTAAACAGAACTCAGCAAACTTCGTA 239
QY 240 tggattgcgtgtttatcaacttttgacatctactcgtggaagccgggtatattg 299
DB 240 TGCATTGCCGGGTTTATCATCTTTGGCATCTATCTCCGGGGAACCCGTTATATTG 299
QY 300 ctcaaatag 309
DB 300 CTCACAATAG 309

RESULT 9

US-09-023-221A-6

Sequence 6, Application US/09023221A

Patent No. 6087128

GENERAL INFORMATION:

APPLICANT: NOLAN, LISA K.

APPLICANT: HORNE, SHELLEY M.

TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MUEITING, RAASCH & GEBHARDT P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: U.S.A.

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,221A

FILING DATE: 12-FEB-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG MS., VICTORIA A.

REGISTRATION NUMBER: 41,287

REFERENCE/DOCKET NUMBER: 255.00010101

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 305-1226

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-023-221A-6

Query Match 81.6%; Score 252; DB 3; Length 309;
Best Local Similarity 88.6%; Pred. No. 1.7e-68;
Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 atcagagataataagatgaaaaaagtatttttcgcgcgtcttgcaagcttattaca 60
DB 1 atcagagataataagatgaaaaaagtatttttcgcgcgtcttgcaagcttattaca 60

QY	1	atcgaggaataataaagatgaaanaaaatgtttcttctgcgcgcctgcgaatgatttttca	60
Db	9295	atcggagataataacccatgaaaaaaaatgctactcgcctacgcgcctgcctgtttttaca	9355
QY	61	ggaatgctcacaacaaacggttactcgtttgnaaacaacgcagcagtaatacaacaaggaa	120
Db	9355	ggaatgctcacaacgagcgtttactcgtttcaaaaacaacgcgcagctagcaccanaagaa	9412
QY	121	accctacatcatattcttcttcggttcgcgggaattggaacaagagaataacttgaatcgacc	180
Db	9415	accctacatcatattcttcttcggtttcgtgaatgagggcagaagaaaaaatctgcagtccacc	9474
QY	181	aaaattgtgtcggttcgagaanaatgtttgttaaaaacgagaacgcagcaaaacttcgtaat	240
Db	9475	aaaattgtgtcggttcgagaanaatgtttgttaaaaacgagaacccagcaaaacttcgtaat	9534
QY	241	ggaatgctcgcgttttatacaattttgtgcatactacatccgcgtggaagcccggttatatgc	300

Db 9535 ggattgctggtttacttacttgaagcatttatacccgctggaagcgctgtatctgc 9594
QY 301 tcacaata 308
Db 9595 tcacaata 9602

RESULT 12
US-09-364-862-13
Sequence 13, Application US/09364862
Patent No. 6221349
GENERAL INFORMATION:
APPLICANT: Couto, Linda B.
APPLICANT: Colosi, Peter C.
TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII
TITLE OF INVENTION: BY TARGET
FILE REFERENCE: AVIGEN-03/743
CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/104,994
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 11933
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-364-862-13

Query Match 81.6%; Score 252; DB 4; Length 11933;
Best Local Similarity 88.6%; Pred. No. 6,6e-68;
Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 atgcagatatataagttgtaaaaaatgtttcttgcgcgtctggaagcattataca 60
Db 9295 atcggaataacacccatgaaaaaatgtctactctgcgtcgcgtccgcttataca 9354
QY 61 ggattgctcaacaacgcttactgttggacaacacccgacagatgacacaaaggaa 120
Db 9355 ggattgctcaacaacgcttactgttcaaaaaaacccgacagatgacacaaaggaa 9414
QY 121 accatcatcatatcttcttctgttcgggaattggacaagaagaacgttgtatgcagcc 180
Db 9415 accatcatcatatcttcttctgttcgggaattggcgagaagaagaacgttgtatgcagcc 9474
QY 181 aaaaattgtggtggtgcagagaatgttgttaaaacagaaactcagcaaatctgttaaat 240
Db 9475 aaaaattgtggtggtgcagagaatgttgttaaaacagaaactcagcaaatctgttaaat 9534
QY 241 ggattgctcggtttacttacttggacatcatctcgcgttggaaagccggtatattgc 300
Db 9535 ggattgctcggtttacttacttgaagcattatacccgctggaagcgctgtatctgc 9594
QY 301 tcacaata 308
Db 9595 tcacaata 9602

RESULT 13
US-09-002-361-4
Sequence 4, Application US/09002361
Patent No. 6329516
GENERAL INFORMATION:
APPLICANT: Halling, Blaik
TITLE OF INVENTION: Lepidopteran GABA-gated Chloride
Channels

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,361
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1443
OTHER INFORMATION:
US-09-002-361-4

Query Match 11.1%; Score 34.2; DB 4; Length 1519;
Best Local Similarity 67.6%; Pred. No. 0.21; Mismatches 23; Indels 0; Gaps 0;
Matches 48; Conservative 0

QY 153 tggacaagaagaacacttgatgagccaaattgtggtggtgcagaaatgtgttaa 212
Db 992 TGGCAAGAGAAATACAGATGAGAAACAAAGATTGTGGCCATACAGAAATAGCTTCTG 1051
QY 213 aacagaacac 223
Db 1052 AAAAGAAATAC 1062

RESULT 14
US-08-743-637B-1
Sequence 1, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: OUBLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN


```

COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1817 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecalis
US-08-743-637B-1

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Query Match          10.9%; Score 33.6; DB 2; Length 1817;
Best Local Similarity 51.3%; Pred. No. 0.34; Mismatches 0; Gaps 0;
Matches 78; Conservative 0; Indels 0;

Qy 127 acatcatcttccttcggttcggaattgacaagaagaactgtgtgacgccaatt 186
Db 1211 ACATATCTTCCTCTTAGATGTAGTGTGTCATGAATGACACATGTCGACGGAACAT 1270
Qy 187 tctggcggctgcagaagaatgtgttaaaacagaaactcagcaaacattcgtaaatgttg 246
Db 1271 ACTGCCGCTTAGAATATTAGACAAATCAGATGCTGAATGAATCTATTCTGATTG 1330
Qy 247 ctgggtttatcaactttggcatctatcc 278
Db 1331 ATGGGTATTATTATTCGGGTGATCTAATCC 1362

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```

RESULT 15
US-08-526-840B-1
Sequence 1, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY GENES
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1817 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecalis
US-08-526-840B-1

```

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Query Match          10.9%; Score 33.6; DB 3; Length 1817;
Best Local Similarity 51.3%; Pred. No. 0.34; Mismatches 0; Gaps 0;
Matches 78; Conservative 0; Indels 0;

Qy 127 acatcatcttccttcggttcggaattgacaagaagaactgtgtgacgccaatt 186
Db 1211 ACATATCTTCCTCTTAGATGTAGTGTGTCATGAATGACACATGTCGACGGAACAT 1270
Qy 187 tctggcggctgcagaagaatgtgttaaaacagaaactcagcaaacattcgtaaatgttg 246
Db 1271 ACTGCCGCTTAGAATATTAGACAAATCAGATGCTGAATGAATCTATTCTGATTG 1330
Qy 247 ctgggtttatcaactttggcatctatcc 278
Db 1331 ATGGGTATTATTATTCGGGTGATCTAATCC 1362

```

Search completed: July 23, 2002, 13:45:10
Job time: 5111 sec

DR WPI: 2000-531343/48.
 DR P-PSDB; AAB14981.

XX Nucleic acid molecule encoding *iss* polypeptide isolated from avian
 PT *Escherichia coli*, used to prevent avian septicemic diseases and for
 PT diagnostic and control strategies for avian colibacillosis

XX Claim 17; Fig 3; 33pp; English.

XX The present invention relates to the avian *Escherichia coli iss* gene.
 CC *iss* encodes an outer membrane protein. This gene was obtained by PCR
 CC amplification of an *E. coli* isolate from chick serum. The present
 CC sequence is the *iss* cDNA as cloned in frame into the expression vector
 CC pGEX-6P-3. The *iss* gene is useful as a vaccine for treating and
 CC preventing avian septicemic diseases and functions as a marker for
 CC diseases causing avian *E. coli* infection. This forms the basis for
 CC improved diagnostic and control strategies for avian colibacillosis.

XX Sequence 309 BP; 101 A; 60 C; 64 G; 84 T; 0 other;

Query Match 100.0%; Score 309; DB 21; Length 309;
 Best Local Similarity 100.0%; Pred. No. 8.4e-80;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atcgagataataagatgaaaaaatttttttcgcgcctctgcaatgctattaca 60
 Db 1 atcgagataataagatgaaaaaatttttttcgcgcctctgcaatgctattaca 60
 QY 61 ggaatgctcaacaacggttactgttggaacaacccgacagatgaacccaagaa 120
 Db 61 ggaatgctcaacaacggttactgttggaacaacccgacagatgaacccaagaa 120
 QY 121 accatcaatcatcattcttcgttcggaattggaacaagaagaactgttgatgacgc 180
 Db 121 accatcaatcatcattcttcgttcggaattggaacaagaagaactgttgatgacgc 180
 QY 181 aaattctgagcggtgcagaaaaatgtgttaaaacagaaactcagaacaattcgttaaat 240
 Db 181 aaattctgagcggtgcagaaaaatgtgttaaaacagaaactcagaacaattcgttaaat 240
 QY 241 ggaatgctcggttttaccattttgcatctatacccgctggaagcccggtatattgc 300
 Db 241 ggaatgctcggttttaccattttgcatctatacccgctggaagcccggtatattgc 300
 QY 301 tcacaataag 309
 Db 301 tcacaataag 309

RESULT 2

AAAF58100
 ID AAF58100 standard; DNA; 309 BP.

XX AAF58100;

XX 04-MAY-2001 (first entry)

DE Avian *E. coli* isolate *iss* gene clone SEQ ID NO: 22.

XX Avian *E. coli* infection; respiratory tract lesion; septicaemia;
 KW colibacillosis; ds.

XX *Escherichia coli*.

XX US6187321-B1.

XX 13-FEB-2001.

XX 31-MAR-1999; 99US-0282352.

XX 12-FEB-1998; 98US-0023221.

PA (UYND-) UNIV NORTH DAKOTA STATE.

XX Nolan LK, Horne SM, Robinson M;

XX WPI: 2001-190978/19.

DR Novel isolated and purified avian *Escherichia coli iss* polypeptide
 XX useful for treating *Escherichia coli* infection selected from
 PT colibacillosis, coliformuloma, peritonitis, salpingitis, synovitis,
 PT omphalitis

XX Example 2; Column 47-48; 35pp; English.

XX The present invention provides the protein and coding sequences of the
 CC *Escherichia coli iss* protein. This can be used in the diagnosis and
 CC treatment of, and vaccines against, *E. coli* infection in domestic birds,
 CC where the bacterium causes septicaemia, respiratory tract lesions and
 CC colibacillosis.

XX Sequence 309 BP; 101 A; 60 C; 64 G; 84 T; 0 other;

Query Match 100.0%; Score 309; DB 22; Length 309;
 Best Local Similarity 100.0%; Pred. No. 8.4e-80;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atcgagataataagatgaaaaaatttttttcgcgcctctgcaatgctattaca 60
 Db 1 atcgagataataagatgaaaaaatttttttcgcgcctctgcaatgctattaca 60
 QY 61 ggaatgctcaacaacggttactgttggaacaacccgacagatgaacccaagaa 120
 Db 61 ggaatgctcaacaacggttactgttggaacaacccgacagatgaacccaagaa 120
 QY 121 accatcaatcatcattcttcgttcggaattggaacaagaagaactgttgatgacgc 180
 Db 121 accatcaatcatcattcttcgttcggaattggaacaagaagaactgttgatgacgc 180
 QY 181 aaattctgagcggtgcagaaaaatgtgttaaaacagaaactcagaacaattcgttaaat 240
 Db 181 aaattctgagcggtgcagaaaaatgtgttaaaacagaaactcagaacaattcgttaaat 240
 QY 241 ggaatgctcggttttaccattttgcatctatacccgctggaagcccggtatattgc 300
 Db 241 ggaatgctcggttttaccattttgcatctatacccgctggaagcccggtatattgc 300
 QY 301 tcacaataag 309
 Db 301 tcacaataag 309

RESULT 3

AAAF73697
 ID AAF73697 standard; DNA; 378 BP.

XX AAF73697;

XX 07-DEC-2000 (first entry)

DE *E. coli iss* gene in expression vector pGEX-6P-3.

XX *iss*; avian; outer membrane protein; OMP; vaccine; antibacterial;
 KW avian colibacillosis; septicemic; pGEX-6P-3; ss.

XX *Escherichia coli*.

XX Key Location/Qualifiers

XX CDS 34..342

XX /tag- a

XX /product- iss

XX US6087128-A.

PD 11-JUL-2000.
XX 12-FEB-1998; 98US-0023221.
XX 12-FEB-1998; 98US-0023221.
XX (NDSU-) NDSU RES FOUND.
XX Nolan LK, Horne SM;
XX WPI; 2000-531343/48.
DR P-PSDB; AAB14984.
XX
XX Nucleic acid molecule encoding Iss polypeptide isolated from avian
PT Escherichia coli, used to prevent avian septicemic diseases and for
DR diagnostic and control strategies for avian colibacillosis
XX
XX Disclosure; Fig 3; 33pp; English.
XX
XX The present invention relates to the avian Escherichia coli Iss gene.
CC Iss encodes an outer membrane protein. This gene was obtained by PCR
CC amplification of an E.coli isolate from chick serum. The present
CC sequence is the Iss gene cloned in frame into the expression vector
CC pGEX-6P-3. The Iss gene is useful as a vaccine for treating and
CC preventing avian septicemic diseases and functions as a marker for
CC diseases causing avian E. coli infection. This forms the basis for
CC improved diagnostic and control strategies for avian colibacillosis.
XX
XX Sequence 378 BP; 112 A; 80 C; 84 G; 102 T; 0 other;
SQ

Query Match 100.0%; Score 309; DB 21; Length 378;
Best Local Similarity 100.0%; Pred. No. 8.9e-80;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atcgcgagataaataagatgataaataatgtattttctgcgcgtctggaatgtattaca 60
DB 34 atcgcgagataaataagatgataaataatgtattttctgcgcgtctggaatgtattaca 93
QY 61 ggaatgtctcaacaacagcttactgttggaacaacacgacagcagtaacacaaagaa 120
DB 94 ggaatgtctcaacaacagcttactgttggaacaacacgacagcagtaacacaaagaa 153
QY 121 accatcacatcatcattctctgttcggaattggaacaagaagaactgtgatcgagcc 180
DB 154 accatcacatcatcattctctgttcggaattggaacaagaagaactgtgatcgagcc 213
QY 181 aaaaatttggcggtgcagaaaatgtttaaacaagaacacacgaacatcgttaaat 240
DB 214 aaaaatttggcggtgcagaaaatgtttaaacaagaacacacgaacatcgttaaat 273
QY 241 ggaatgtctggtttatcaacttttggaatctactcgcgtggaagccgggtatattgc 300
DB 274 ggaatgtctggtttatcaacttttggaatctactcgcgtggaagccgggtatattgc 333
QY 301 tcacaataag 309
DB 334 tcacaataag 342

RESULT 4
AAF58800
ID AAF58800 standard; DNA; 378 BP.
XX
AC AAF58800;

XX 04-MAY-2001 (first entry)
XX
XX Avian E coli isolate protease cleavage site DNA SEQ ID NO: 21.
DE
XX Avian E coli infection; respiratory tract lesion; septicemia;
KW colibacillosis; ds.
XX

OS Escherichia coli.
XX
XX US6187321-B1.
XX
XX 13-FEB-2001.
XX
XX 31-MAR-1999; 99US-0282352.
XX
XX 12-FEB-1998; 98US-0023221.
XX
XX (UYND-) UNIV NORTH DAKOTA STATE.
XX Nolan LK, Horne SM, Robinson M;
XX WPI; 2001-190978/19.
DR P-PSDB; AAB69397.
XX
XX Novel isolated and purified avian Escherichia coli Iss polypeptide
PT useful for treating Escherichia coli infection selected from
PT colibacillosis, coligranuloma, peritonitis, salpingitis, synovitis,
PT omphalitis
XX
XX Example 2; Column 47-48; 35pp; English.
XX
XX The present invention provides the protein and coding sequences of the
CC Escherichia coli Iss protein. This can be used in the diagnosis and
CC treatment of, and vaccines against, E. coli infection in domestic birds,
CC where the bacterium causes septicemia, respiratory tract lesions and
CC colibacillosis.
XX
XX Sequence 378 BP; 112 A; 80 C; 84 G; 102 T; 0 other;
SQ

Query Match 100.0%; Score 309; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 8.9e-80;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atcgcgagataaataagatgataaataatgtattttctgcgcgtctggaatgtattaca 60
DB 34 atcgcgagataaataagatgataaataatgtattttctgcgcgtctggaatgtattaca 93
QY 61 ggaatgtctcaacaacagcttactgttggaacaacacgacagcagtaacacaaagaa 120
DB 94 ggaatgtctcaacaacagcttactgttggaacaacacgacagcagtaacacaaagaa 153
QY 121 accatcacatcatcattctctgttcggaattggaacaagaagaactgtgatcgagcc 180
DB 154 accatcacatcatcattctctgttcggaattggaacaagaagaactgtgatcgagcc 213
QY 181 aaaaatttggcggtgcagaaaatgtttaaacaagaacacacgaacatcgttaaat 240
DB 214 aaaaatttggcggtgcagaaaatgtttaaacaagaacacacgaacatcgttaaat 273
QY 241 ggaatgtctggtttatcaacttttggaatctactcgcgtggaagccgggtatattgc 300
DB 274 ggaatgtctggtttatcaacttttggaatctactcgcgtggaagccgggtatattgc 333
QY 301 tcacaataag 309
DB 334 tcacaataag 342

RESULT 5
AAA73681
ID AAA73681 standard; DNA; 760 BP.
XX
AC AAA73681;

XX 07-DEC-2000 (first entry)
XX
XX Avian Escherichia coli Iss gene.
DE
XX Iss; avian; outer membrane protein; OMP; vaccine; antibacterial;
KW
XX

RESULT 7
 AAA73684 standard; cDNA; 309 BP.
 ID AAA73684
 AC AAA73684;
 XX
 XX 07-DEC-2000 (first entry)
 DE Is cDNA from a septicemic human E.coli isolate.
 XX
 XX Is; avian; outer membrane protein; OMP; vaccine; antibacterial;
 KM avian colibacillosis; septicemic; human; ss.
 XX
 XX Escherichia coli.
 OS
 XX
 XX Key Location/Qualifiers
 XX CDS 1..309
 XX /*tag- a
 XX /product- iss

US6087128-A.
 11-JUL-2000.
 12-FEB-1998; 98US-0023221.
 12-FEB-1998; 98US-0023221.
 (NDSU-) NDSU RES FOUND.
 Nolan LK, Horne SM;
 WPI: 2000-531343/48.
 P-PSDB: AABI4982.

Nucleic acid molecule encoding iss polypeptide isolated from avian
 Escherichia coli, used to prevent avian septicemic diseases and for
 diagnostic and control strategies for avian colibacillosis

PS Disclosure; Fig 1; 33pp; English.
 XX
 XX The present invention relates to the avian Escherichia coli iss gene.
 CC iss encodes an outer membrane protein. This gene was obtained by PCR
 CC amplification of an E.coli isolate from chick serum. The present
 CC sequence is the iss gene from a septicemic human E.coli isolate,
 CC which shows homology to the avian E. coli iss gene. The iss
 CC gene is useful as a vaccine for treating and preventing avian
 CC septicemic diseases and functions as a marker for diseases causing
 CC avian E. coli infection. This forms the basis for improved diagnostic
 CC and control strategies for avian colibacillosis.

Sequence 309 BP; 101 A; 65 C; 59 G; 84 T; 0 other;

Query Match 88.4%; Score 273.2; DB 21; Length 309;
 Best Local Similarity 96.8%; Pred. NO. 1.9e-69;
 Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

OY 1 atgcagagataaagaatgaataaataatgtattcttcgtccgctctggaatgcttattaca 60
 DB 1 atgcagagataaagaatgaataaataatgtattcttcgtccgctctggaatgcttattaca 60
 OY 61 ggaatgctcaacaacagttactctgttggaacaaacgacagcagtaacacaaagga 120
 DB 61 ggaatgctcaacaacagttactctgttggaacaaacgacagcagtaacacaaagga 120
 OY 121 accatcactacatcttcttcgttcgggaattggaacaaaggaactgtgatgagcc 180
 DB 121 accatcactacatcttcttcgttcgggaattggaacaaaggaactgtgatgagcc 180
 OY 121 accatcactacatcttcttcgttcgggaattggaacaaaggaactgtgatgagcc 180
 DB 121 accatcactacatcttcttcgttcgggaattggaacaaaggaactgtgatgagcc 180
 OY 181 aaatttg-tggcggtgcagaaatggttttaaacagaaactcgcaacttctgttaa 239
 DB 181 aaatttg-tggcggtgcagaaatggttttaaacagaaactcgcaacttctgttaa 239

OY 240 tgaattgctcgtgtttatcacttttgcatctatactccgctggaagccggtatattg 299
 DB 240 tgaattgctcgtgtttatcacttttgcatctatactccgctggaagccggtatattg 299
 OY 300 ctcaacataag 309
 DB 300 ctcaacataag 309

RESULT 8
 AAF58787 standard; DNA; 309 BP.
 ID AAF58787
 AC AAF58787;
 XX
 XX 04-MAY-2001 (first entry)
 DE Human E coli isolate iss gene SEQ ID NO: 5.
 XX
 XX
 XX Human E coli isolate; respiratory tract lesion; septicemia;
 KM Avian E coli infection; respiratory tract lesion; septicemia;
 XX colibacillosis; ds.
 OS
 XX Escherichia coli.
 OS
 XX
 XX US6187321-B1.
 13-FEB-2001.
 31-MAR-1999; 99US-0282352.
 12-FEB-1998; 98US-0023221.
 (UYND-) UNIV NORTH DAKOTA STATE.
 Nolan LK, Horne SM, Robinson M;
 WPI: 2001-190978/19.

Novel isolated and purified avian Escherichia coli iss polypeptide
 useful for treating Escherichia coli infection selected from
 colibacillosis, coligranuloma, peritonitis, salpingitis, synovitis,
 omphalitis

Example 1; Column 39-40; 35pp; English.

XX The present invention provides the protein and coding sequences of the
 CC Escherichia coli iss protein. This can be used in the diagnosis and
 CC treatment of, and vaccines against, E. coli infection in domestic birds,
 CC where the bacterium causes septicemia, respiratory tract lesions and
 CC colibacillosis.

Sequence 309 BP; 101 A; 65 C; 59 G; 84 T; 0 other;

Query Match 88.4%; Score 273.2; DB 22; Length 309;
 Best Local Similarity 96.8%; Pred. NO. 1.9e-69;
 Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

OY 1 atgcagagataaagaatgaataaataatgtattcttcgtccgctctggaatgcttattaca 60
 DB 1 atgcagagataaagaatgaataaataatgtattcttcgtccgctctggaatgcttattaca 60
 OY 61 ggaatgctcaacaacagttactctgttggaacaaacgacagcagtaacacaaagga 120
 DB 61 ggaatgctcaacaacagttactctgttggaacaaacgacagcagtaacacaaagga 120
 OY 121 accatcactacatcttcttcgttcgggaattggaacaaaggaactgtgatgagcc 180
 DB 121 accatcactacatcttcttcgttcgggaattggaacaaaggaactgtgatgagcc 180
 OY 121 accatcactacatcttcttcgttcgggaattggaacaaaggaactgtgatgagcc 180
 DB 121 accatcactacatcttcttcgttcgggaattggaacaaaggaactgtgatgagcc 180
 OY 181 aaatttg-tggcggtgcagaaatggttttaaacagaaactcgcaacttctgttaa 239
 DB 181 aaatttg-tggcggtgcagaaatggttttaaacagaaactcgcaacttctgttaa 239

Db 61 ggaatgctcacaacagcttactgttcaaaaacaaccgcagcatgaccacaagaagaa 120
Qy 121 accacactcatcatcttcgtttccgggaatttgacagaagaaaaactgttagcgacc 180
Db 122 accacaccacatcatcttcgtttccgggaatttgacagaagaaaaactgttagcgacc 180
Qy 181 aaattctgvcgvcgtgcagaaaatgttgttaaacagaaaactcagcaaatctgtaat 240
Db 181 aaattctgvcgvcgagaaaatgttgttaaacagaaaactcagcaaatctgtaat 240
Qy 241 ggattgcccggtttatatctttggcatctatactccgctgcgaagccgggtatattgc 300
Db 241 ggattgcccggtttatatctttaggcatcttatactccgctgcgaagcgvtglatgc 300
Qy 301 tcacata 308
Db 301 tcacata 308

RESULT 10
ID AAF58788 standard; DNA; 309 BP.
AC AAF58788;
XX
DT 04-MAY-2001 (first entry)
DE Phage lambda bor gene SEQ ID NO: 6.
KW Avian E coli infection; respiratory tract lesion; septicaemia;
collibacillosis; ds.
OS Bacteriophage lambda.
XX US6187321-B1.
XX
PD 13-FEB-2001.
XX
PF 31-MAR-1999; 99US-0282352.
XX
PR 12-FEB-1998; 98US-0023221.
XX
PA (UYND-) UNIV NORTH DAKOTA STATE.
XX
PI Nolan LK, Horne SM, Robinson M,
DR WPI; 2001-190978/19.
XX
XX Novel isolated and purified avian Escherichia coli fss polypeptide
PT useful for treating Escherichia coli infection selected from
PT colibacillosis, coligranuloma, peritonitis, salpingitis, synovitis,
FT omphalitis
XX
PS Example 1; Column 39-40; 35pp; English.

The present invention provides the protein and coding sequences of the
Escherichia coli fss protein. This can be used in the diagnosis and
treatment of, and vaccines against, E. coli infection in domestic birds,
where the bacterium causes septicaemia, respiratory tract lesions and
colibacillosis.

FN 00200100/2 541
XX

XX
PD 11-OCT-2001.
XX

PD	11-OCT-2001.
,XX	
PF	30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 DR WPI; 2001-639362/73.
 XX P-PSDB: ABG29752.
 DR
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

Claim 1; SEQ ID No 29743; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SO Sequence 1023 BP; 272 A; 267 C; 267 G; 217 T; 0 other;

Query Match 12.6%; Score 39; DB 23; Length 1023;
 Best Local Similarity 81.8%; Pred. No. 0.14;
 Matches 45; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 29 tattctctccgctctggcaatgcttattacagatgctcacaacgctttac 83
 |||||
 DB 1022 TACTCGCTACTGCGCTGCGCTCTATTACAGATGCTCTCAACACATTATAC 968

RESULT 15

AAA26702
 ID AAA26702 standard; CDNA; 1685 BP.

XX AAA26702;

XX 23-JUN-2000 (first entry)

XX Candida albicans polynucleotide sequence #40.

XX Candida albicans infection; growth; survival; medication; AIDS;

XX vulvovaginitis; immunocompromised patient; treat; ss.

XX Candida albicans.

XX EP982401-A2.

XX 01-MAR-2000.

XX 23-DEC-1998; 98EP-0310694.

PR 14-AUG-1998; 98GB-0017796.
 XX
 XX (JANC) JANSSEN PHARM NV.
 XX
 XX Contreras RH, Nelissen B, De Backer MD, Luyten WHML, Vlaene JE;
 PI Logghe MG;
 DR WPI; 2000-258614/23.
 XX
 PT Essential polypeptides isolated from Candida albicans, useful in the
 PT treatment of diseases caused by C. albicans, especially in
 PT immunocompromised subjects, e.g., AIDS patients
 PS
 XX Claim 1; Page 78; 133pp; English.

XX This sequence represents a polynucleotide sequence encoding a polypeptide
 CC that is critical for the survival and growth of Candida albicans. The
 CC C. albicans nucleic acid molecules of the invention may be used as probes
 CC and primers for detecting homologous nucleic acid molecule sequences.
 CC The polypeptides and nucleic acid molecules and compounds identified as
 CC selectively modulating the expression of the polypeptides, may be used as
 CC medications or for the preparation of a medication to treat C. albicans
 CC associated diseases, especially in AIDS patients and to treat
 CC vulvovaginitis in otherwise healthy females. The use of the polypeptides
 CC and polynucleotide sequences to treat C. albicans associated diseases has
 CC fewer side effects and less toxicity than previously used methods such as
 CC the use of amphotericin. This method is therefore especially suitable for
 CC immunocompromised patients, such as AIDS patients.
 XX

SO Sequence 1685 BP; 650 A; 281 C; 250 G; 504 T; 0 other;

Query Match 11.7%; Score 36.2; DB 21; Length 1685;
 Best Local Similarity 59.0%; Pred. No. 1;
 Matches 62; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

OY 109 aacacaaaggaaccatcacatcatcttcgttcggaattggaagaagaact 168
 |||||
 DB 1334 aacacacgcgaaaccacacattataatcatcgcgctagatgagaagaagtgaatt 1393

OY 169 gttgatgcagcacaattgtggtcggtgcagaaatgttgttaa 213
 |||||
 DB 1394 agtgatgatgagtttattcttgatgagaagaatgaaatattgaa 1438

Search completed: July 23, 2002, 13:51:29
 Job time: 5380 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 13:43:18 ; Search time 1949.42 Seconds
(without alignments)
3317.038 Million cell updates/sec

Title: US-09-738-599-22

Perfect score: 1 atgcagagataataagatgaa.....gggtatattgtccacataag 309

Sequence: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

1	309	100.0	309	6	AR102880	Sequence
2	309	100.0	309	6	AR129424	Sequence
3	309	100.0	378	6	AR102879	Sequence
4	309	100.0	378	6	AR129423	Sequence
5	309	100.0	760	6	AF042279	Escherich
6	309	100.0	760	6	AR102863	Sequence
7	309	100.0	760	6	AR129407	Sequence
8	273.2	88.4	309	6	AR102866	Sequence
9	273.2	88.4	309	6	AR129410	Sequence
10	273.2	88.4	1330	6	ECISSEGENE	X52665 E.coli DNA
11	252	81.6	309	6	AR102867	Sequence
12	252	81.6	309	6	AR129411	Sequence
13	252	81.6	326	7	BLANLON	X53792 Bacterioph
14	252	81.6	9170	12	002453	U02427 Cloning vec
15	252	81.6	9205	12	XX002427	U02427 Cloning vec
16	252	81.6	11313	6	AE005297	AE005297 Escherich
17	252	81.6	11933	6	AR138377	AR138377 Sequence
18	252	81.6	11933	6	AR146887	AR146887 Sequence
19	252	81.6	42539	12	CV039284	CV039284
20	252	81.6	42530	12	CV039285	CV039285
21	252	81.6	42531	12	CV039286	CV039286
22	252	81.6	42704	12	CV037692	CV037692
23	252	81.6	48502	7	LAMCG	J02459 Bacterioph
24	252	81.6	61670	7	AF125520	AF125520 Bacterioph
25	252	81.6	65510	1	AP000422	AP000422 Escherich
26	252	81.6	327773	1	AP002554	AP002554 Escherich
27	247.2	80.0	14164	1	AE005330	AE005330 Escherich
28	247.2	80.0	16170	1	AE000161	AE000161 Escherich
29	247.2	80.0	136742	1	EC082598	EC082598 Escherich
30	247.2	80.0	222605	1	AP002555	AP002555 Escherich
31	141.6	45.8	180	1	AF222286	AF222286 Escherich
32	141.6	45.8	180	6	AX275633	AX275633 Sequence
33	141.2	45.7	752	8	AF441251	AF441251 Paracocc
34	45.2	14.6	182116	9	AC093831	AC093831 Homo sapi
35	43	13.9	117864	9	AC096950	AC096950 Homo sapi
36	43	13.9	148224	2	AC009418	AC009418 Homo sapi
37	43	13.9	164132	2	AC019284	AC019284 Homo sapi
38	43	13.9	165947	2	AC015897	AC015897 Homo sapi
39	41	13.3	109894	2	AC074132	AC074132 Homo sapi
40	41	13.3	142116	9	AC034215	AC034215 Homo sapi
41	40.8	13.2	97451	8	F19K23	AC000375 Sequence
42	39.2	12.7	110611	8	AC022520	AC022520 Arabidops
43	39.2	12.7	130235	8	AC008007	AC008007 Genomic s
44	38.8	12.6	55341	2	AC102312	AC102312 Mus muscu
45	38.8	12.6	159981	2	AC069074	AC069074 Mus muscu

ALIGNMENTS

RESULT	1	309 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR102880				
DEFINITION	Sequence 22 from patent US 6087128.				
ACCESSION	AR102880				
VERSION	AR102880.1	GI:12814468			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 309)				
AUTHORS	Nolan, L.K. and Horne, S.M.				
TITLE	DNA encoding an avian E. coli 1ss				
JOURNAL	Patent: US 6087128-A 22 11-JUL-2000;				
FEATURES	location/Qualifiers				
source	1..309				
BASE COUNT	101 a	60 c	64 g	84 t	
ORIGIN	/organism="unknown"				

Query Match 100.0%; Score 309; DB 6; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.6e-68;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 301 TCACAAATAG 309

RESULT 2
LOCUS AR129424 309 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6187321.
ACCESSION AR129424
VERSION AR129424.1 GI:14117321
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 309)
AUTHORS Nolan, L.K., Horne, S.M. and Robinson, M.
TITLE Avian E. coli 1ss polypeptide
JOURNAL Patent: US 6187321-A 22 13-FEB-2001;
FEATURES
Location/Qualifiers
1..309
BASE COUNT 101 a 60 c 64 g 84 t
ORIGIN

Query Match 100.0%; Score 309; DB 6; Length 309;
Best Local Similarity 100.0%; Pred. No. 2,6e-68;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 301 TCACAAATAG 309

RESULT 3
LOCUS AR102879 378 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 21 from patent US 6087128.
ACCESSION AR102879
VERSION AR102879.1 GI:12814467
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 378)
AUTHORS Nolan, L.K. and Horne, S.M.
TITLE DNA encoding an avian E. coli 1ss
JOURNAL Patent: US 6087128-A 21 11-JUL-2000;
FEATURES
Location/Qualifiers
1..378
BASE COUNT 112 a 80 c 84 g 102 t
ORIGIN

Query Match 100.0%; Score 309; DB 6; Length 378;
Best Local Similarity 100.0%; Pred. No. 2,6e-68;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 301 TCACAAATAG 309

RESULT 4
LOCUS AR129423 378 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 21 from patent US 6187321.
ACCESSION AR129423
VERSION AR129423.1 GI:14117320
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 378)
AUTHORS Nolan, L.K., Horne, S.M. and Robinson, M.
TITLE Avian E. coli 1ss polypeptide
JOURNAL Patent: US 6187321-A 21 13-FEB-2001;
FEATURES
Location/Qualifiers
1..378
BASE COUNT 112 a 80 c 84 g 102 t
ORIGIN

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 301 TCACAAATAG 309

RESULT 3
LOCUS AR102879 378 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 21 from patent US 6087128.
ACCESSION AR102879
VERSION AR102879.1 GI:12814467
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 378)
AUTHORS Nolan, L.K. and Horne, S.M.
TITLE DNA encoding an avian E. coli 1ss
JOURNAL Patent: US 6087128-A 21 11-JUL-2000;
FEATURES
Location/Qualifiers
1..378
BASE COUNT 112 a 80 c 84 g 102 t
ORIGIN

Query Match 100.0%; Score 309; DB 6; Length 378;
Best Local Similarity 100.0%; Pred. No. 2,6e-68;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 301 TCACAAATAG 309

RESULT 4
LOCUS AR129423 378 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 21 from patent US 6187321.
ACCESSION AR129423
VERSION AR129423.1 GI:14117320
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 378)
AUTHORS Nolan, L.K., Horne, S.M. and Robinson, M.
TITLE Avian E. coli 1ss polypeptide
JOURNAL Patent: US 6187321-A 21 13-FEB-2001;
FEATURES
Location/Qualifiers
1..378
BASE COUNT 112 a 80 c 84 g 102 t
ORIGIN

Query Match 100.0%; Score 309; DB 6; Length 378;
 Best Local Similarity 100.0%; Pred. No. 2,5e-68;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgcagagataaagaatgaaataatgttattcttcgctcgttcgcaatgcttattaca 60
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 Db 34 ATCAGAGATATATAGATGAAAAAATGTATTTCTGCGCCTGCGCAATGCTTATACA 93
 QY 61 ggtgtgctcaacaacagtttactgttggaaacacacagcaatcaacccaagaagaa 120
 |||||
 Db 94 GGATGTGCTCAACAAACGTTTACTGTGGAAACAAACCGACACAGATTAACCAAGAA 153
 QY 121 accatcacatcatcttcttcgttcggaattggacaagaagaactgttgatgcagcc 180
 |||||
 Db 154 ACCATCATCATCATTTCTTCTGTTGGAAATGGACAAAGAACTGTGTATGACAGCC 213
 QY 181 aaaaattgtgcyggtgcagaaaatgtttaaacaagaaactcaagaacattcgtaaat 240
 |||||
 Db 214 AAAATTGTGCGCGTCAAGAAATGTTTAAACAGAAACTCAGCAAACTTCGTAAAT 273
 QY 241 ggtgtgctcggtttatcaacttttgcatctatactccgctggaagccgggtatattgc 300
 |||||
 Db 274 GGATGTGCTCGGTTTATCACTTTGGCATCTATATCTCCGCTGGAAGCCCGGTATATTC 333
 QY 301 tcacaatag 309
 |||||
 Db 334 TCACATAG 342

RESULT 5
 AF042279 760 bp DNA linear BCT 18-SEP-2001
 LOCUS Escherichia coli 1ss (1ss) gene, complete cds.
 DEFINITION AF042279
 ACCESSION AF042279.1 GI:5305229
 VERSION AF042279.1
 KEYWORDS Escherichia coli.
 SOURCE Escherichia coli.
 ORGANISM Escherichia coli.
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

REFERENCE 1 (bases 1 to 760)
 AUTHORS Horne,S.M., Pfaff-McDonough,S.J., Giddings,C.W. and Nolan,L.K.
 TITLE Cloning and sequencing of the 1ss gene from a virulent avian
 Escherichia coli
 JOURNAL Avian Dis. 44 (1), 179-184 (2000)
 MEDLINE 20199920
 PUBMED 10737659
 REFERENCE 2 (bases 1 to 760)
 AUTHORS Horne,S.M., Nolan,L.K., Giddings,C.W. and Pfaff,S.J.
 TITLE Direct Submision
 JOURNAL Submitted (10-JAN-1998) Vet. & Micro. Sci., North Dakota State
 Univ., Van Es Hall, Fargo, ND 58105, USA
 FEATURES
 source
 1..760
 /organism="Escherichia coli"
 /strain="102"
 /db_xref="taxon:562"
 /note="may be on a large R plasmid"
 292..600
 /gene="1ss"
 292..600
 /gene="1ss"
 /note="similar to Bacteriophage lambda Bor protein, and to
 1ss protein from a septicemic human Escherichia coli
 isolate; causes avian colibacillosis"
 /codon_start=1
 /transl_table=11
 /product="1ss"
 /protein_id="AAD41540.1"
 /db_xref="GI:5305230"
 /translation="MODNMKMKMLFSALAMLTITGCAQOTFTVGNKPTAVTPRETTTH

HEFVSGIGQETVDAKICGGAENVKTEPQTFVNGLIGETTFG
 BASE COUNT 216 a 159 c 160 g 225 t
 ORIGIN

Query Match 100.0%; Score 309; DB 1; Length 760;
 Best Local Similarity 100.0%; Pred. No. 2,5e-68;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgcagagataaagaatgaaataatgttattcttcgctcgttcgcaatgcttattaca 60
 |||||
 Db 292 ATCAGAGATATATAGATGAAAAAATGTATTTCTGCGCCTGCGCAATGCTTATACA 351
 QY 61 ggtgtgctcaacaacagtttactgttggaaacacacagcaatcaacccaagaagaa 120
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 Db 352 GGATGTGCTCAACAAACGTTTACTGTGGAAACAAACCGACACAGATTAACCAAGAA 411
 QY 121 accatcacatcatcttcttcgttcggaattggacaagaagaactgttgatgcagcc 180
 |||||
 Db 412 ACCATCATCATCATTTCTTCTGTTGGAAATGGACAAAGAACTGTGTATGACAGCC 471
 QY 181 aaaaattgtgcyggtgcagaaaatgtttaaacaagaaactcaagaacattcgtaaat 240
 |||||
 Db 472 AAAATTGTGCGCGTCAAGAAATGTTTAAACAGAAACTCAGCAAACTTCGTAAAT 531
 QY 241 ggtgtgctcggtttatcaacttttgcatctatactccgctggaagccgggtatattgc 300
 |||||
 Db 532 GGATGTGCTCGGTTTATCACTTTGGCATCTATATCTCCGCTGGAAGCCCGGTATATTC 591
 QY 301 tcacaatag 309
 |||||
 Db 592 TCACATAG 600

RESULT 6
 AR102863 760 bp DNA linear PAT 14-FEB-2001
 LOCUS AR102863
 DEFINITION Sequence 1 from patent US 6087128.
 ACCESSION AR102863
 VERSION AR102863.1 GI:12814451
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 Bacteria; Unclassified.
 REFERENCE 1 (bases 1 to 760)
 AUTHORS Nolan,L.K. and Horne,S.M.
 TITLE DNA encoding an avian E. coli 1ss
 JOURNAL Patent: US 6087128-A 1 11-JUL-2000;
 FEATURES
 source
 1..760
 /organism="unknown"
 BASE COUNT 216 a 159 c 160 g 225 t
 ORIGIN

Query Match 100.0%; Score 309; DB 6; Length 760;
 Best Local Similarity 100.0%; Pred. No. 2,5e-68;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgcagagataaagaatgaaataatgttattcttcgctcgttcgcaatgcttattaca 60
 |||||
 Db 292 ATCAGAGATATATAGATGAAAAAATGTATTTCTGCGCCTGCGCAATGCTTATACA 351
 QY 61 ggtgtgctcaacaacagtttactgttggaaacacacagcaatcaacccaagaagaa 120
 |||||
 Db 352 GGATGTGCTCAACAAACGTTTACTGTGGAAACAAACCGACACAGATTAACCAAGAA 411
 QY 121 accatcacatcatcttcttcgttcggaattggacaagaagaactgttgatgcagcc 180
 |||||
 Db 412 ACCATCATCATCATTTCTTCTGTTGGAAATGGACAAAGAACTGTGTATGACAGCC 471
 QY 181 aaaaattgtgcyggtgcagaaaatgtttaaacaagaaactcaagaacattcgtaaat 240

Db 472 AAAATTGTGGCGGTGCGAAGAAATGTTTAAACAGAACTCAGACCAACATTCCTTAAT 531
Qy 241 ggaatgctcgggtttatcaacttttgacatctactcgcgtggaagcccggtatattgc 300
Db 532 GGATGTGCTCGGTTTATACATTGTGGCATCTATACCTCCGCTGGAAGCCCGGTATATTGC 591
Qy 301 tcacaatag 309
Db 592 TCACAATAG 600

RESULT 7
ARI29407
LOCUS ARI29407 760 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6187321.
ACCESSION ARI29407
VERSION ARI29407.1 GI:14117304
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 760)
TITLE Nolan, L.K., Horne, S.M. and Robinson, M.
JOURNAL Avian E. coli 1ss polypeptide
Patent: US 6187321-A 1 13-FEB-2001;
FEATURES
source 1..760
Location/Qualifiers
BASE COUNT 216 a 159 c 160 g 225 t
ORIGIN

Query Match 100.0%; Score 309; DB 6; Length 760;
Best Local Similarity 100.0%; Pred. No. 2.5e-68;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atcgagataataagatgagaaaaatgtattctctcgcgtctggcaatgctattaca 60
Db 292 ATGCAGGATTAATAGATGAAAAAATGTTATTTCTCGCGCTGCAATGCTTATTAACA 351
Qy 61 ggaatgctcacaacagttactcgtttgaaacacacagcagcagtaaccacaaagaa 120
Db 352 GGAATGTGCTCAACAACCTTTACTGTGGAAACAAACCGACAGCGATACACCAAGGAA 411
Qy 121 accatcaatcatctctctcgtttcggtggaattgacaagagaactggtgagcagcc 180
b 412 ACCATCACTCATCTATTTCTTCTTCGGAATGGAACAAGAAAACTGTGATGACAGCC 471
Qy 181 aaaaatgtgagcggtgcagaaaatgtgttaaaacagaactcagcaacattcgtaaat 240
Db 472 AAAATTTGTGCGGTGCGAAGAAATGTTTAAACAGAACTCAGCAAACTTCGTAAAT 531
Qy 241 ggaatgctcgggtttatcaacttttgacatctactcgcgtggaagcccggtatattgc 300
Db 532 GGATGTGCTCGGTTTATACATTGTGGCATCTATACCTCCGCTGGAAGCCCGGTATATTGC 591
Qy 301 tcacaatag 309
Db 592 TCACAATAG 600

RESULT 8
ARI02866
LOCUS ARI02866 309 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6087128.
ACCESSION ARI02866
VERSION ARI02866.1 GI:12814454
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 309)
TITLE Nolan, L.K., Horne, S.M. and Robinson, M.
JOURNAL Avian E. coli 1ss polypeptide
Patent: US 6087128-A 5 11-JUL-2000;
FEATURES
source 1..309
Location/Qualifiers
BASE COUNT 101 a 65 c 59 g 84 t
ORIGIN

AUTHORS Nolan, L.K. and Horne, S.M.
TITLE DNA encoding an avian E. coli 1ss
JOURNAL Patent: US 6087128-A 5 11-JUL-2000;
FEATURES
source 1..309
Location/Qualifiers
BASE COUNT 101 a 65 c 59 g 84 t
ORIGIN

Query Match 88.4%; Score 273.2; DB 6; Length 309;
Best Local Similarity 96.8%; Pred. No. 3.2e-59;
Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

Qy 1 atcgagataataagatgagaaaaatgtattctctcgcgtctggcaatgctattaca 60
Db 1 ATGCAGGATTAATAGATGAAAAAATGTTATTTCTCGCGCTGCAATGCTTATTAACA 60
Qy 61 ggaatgctcacaacagttactcgtttgaaacacacagcagcagtaaccacaaagaa 120
Db 61 GGAATGTGCTCAACAACCTTTACTGTGGAAACAAACCGACAGCATGATGACAGGAA 120
Qy 121 accatcaatcatctctctcgtttcggtggaattgacaagagaactggtgagcagcc 180
Db 121 ACCATCACTCATCTATTTCTTCTTCGGAATGGAACAAGAAAACTGTGATGACAGCC 179
Qy 181 aaaaatgtgagcggtgcagaaaatgtgttaaaacagaactcagcaacattcgtaaa 239
Db 180 AAAATTTGTGCGGTGCGAAGAAATGTTTAAACAGAACTCAGCAAACTTCGTAAAT 239
Qy 240 tgaatgctcgggtttatcaacttttgacatctactcgcgtggaagcccggtatattgc 299
Db 240 TGCAATGCCCGGTTTATACATTGTGGCATCTATACCTCCGCGGGAACCGGTATATTG 299
Qy 300 tcacaatag 309
Db 300 CTCACAATAG 309

RESULT 9
ARI29410
LOCUS ARI29410 309 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6187321.
ACCESSION ARI29410
VERSION ARI29410.1 GI:14117307
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 309)
TITLE Nolan, L.K., Horne, S.M. and Robinson, M.
JOURNAL Avian E. coli 1ss polypeptide
Patent: US 6187321-A 5 13-FEB-2001;
FEATURES
source 1..309
Location/Qualifiers
BASE COUNT 101 a 65 c 59 g 84 t
ORIGIN

Query Match 88.4%; Score 273.2; DB 6; Length 309;
Best Local Similarity 96.8%; Pred. No. 3.2e-59;
Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

Qy 1 atcgagataataagatgagaaaaatgtattctctcgcgtctggcaatgctattaca 60
Db 1 ATGCAGGATTAATAGATGAAAAAATGTTATTTCTCGCGCTGCAATGCTTATTAACA 60
Qy 61 ggaatgctcacaacagttactcgtttgaaacacacagcagcagtaaccacaaagaa 120
Db 61 GGAATGTGCTCAACAACCTTTACTGTGGAAACAAACCGACAGCATGATGACAGGAA 120
Qy 121 accatcaatcatctctcgtttcggtggaattgacaagagaactggtgagcagcc 180

DB 121 ACCATCAGCATCATTTCTTCCTCCCAATGAGC-AGAGAAAAGCTTGATGAGCC 179
 OY 181 aaatttg-tggcgggtgcagaaaatgtgttaaacagaaactgcgaacttgtaaa 239
 DB 180 AAAATTGTTGGCGGTGAGAAAATGTTTAAACAGAACTGACCAAACTTGCTAAA 239
 OY 240 tggattgcgcggttttatacactttgcacatactacgcgcgtggaagccgggtatgt 299
 DB 240 TGCATTGCCGGGTTTATCATTGTCATCTACTCTCGCGGGAACCCGCTGATATTG 299
 OY 300 ctcaaatag 309
 DB 300 CTCACAAATAG 309
 RESULT 10
 ECISSEGENE 1430 bp DNA linear BCT 23-JAN-1992
 LOCUS E.coli DNA for 1ss gene, a plasmid determinant coding for increased
 DEFINITION serum survival and surface exclusion.
 ACCESSION X52665
 VERSION X52665.1 GI:41843
 KEYWORDS 1ss gene.
 SOURCE Escherichia coli.
 ORGANISM Escherichia coli.
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia.
 1 (bases 1 to 1430)
 Chanda, P.J., Leon, M.A., Banerjee, A. and Palchaudhuri, S.
 Cloning and DNA sequence of plasmid determinant 1ss, coding for
 increased serum survival and surface exclusion, which has homology
 with lambda DNA
 Mol. Gen. Genet. 216 (2-3), 287-292 (1989)
 JOURNAL
 MEDLINE
 FEATURES
 SOURCE Location/Qualifiers
 1. 1430
 /organism="Escherichia coli"
 /db_xref="taxon:562"
 BASE COUNT 401 a 313 c 299 g 417 t
 ORIGIN
 Query Match 88.4%; Score 273.2; DB 1; Length 1430;
 Best Local Similarity 96.8%; Pred. No. 2,9e-59;
 Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
 OY 1 atgcaggaataaagaatgaataaataatgttatttctgcgcgtctgcgaatgttataca 60
 DB 770 ATGCAGGATTAATTAAGATGAATAAATGTTATTTCTGCCGCTCGCAATGCTTATTACA 829
 OY 61 ggaatggtcccaacaacgcttactgttgaacaacaacgcagcagtaacacaaaggaa 120
 DB 830 GGATGTGCTCAACAAACGTTTACTGTGGAACAAACCAACCACTAACCACAAAGGAA 889
 OY 121 accatcacatcatattcttcgttcggaattggaacaagaagaactgttgtagcc 180
 DB 890 ACCATCACATCATTTCTTCCTCCCAATGAGC-AGAGAAAAGCTTGATGAGCC 948
 OY 181 aaatttg-tggcgggtgcagaaaatgtgttaaacagaaactgcgaacttgtaaa 239
 DB 949 AAAATTGTTGGCGGTGAGAAAATGTTTAAACAGAACTGACCAAACTTGCTAAA 1008
 OY 240 tggattgcgcggttttatacactttgcacatactacgcgcgtggaagccgggtatgt 299
 DB 1009 TGCATTGCCGGGTTTATCATTGTCATCTACTCTCGCGGGAACCCGCTGATATTG 1068
 OY 300 ctcaaatag 309
 DB 1069 CTCACAAATAG 1078
 RESULT 11

ARI02867
 LOCUS ARI02867 309 bp DNA linear
 DEFINITION Sequence 6 from patent US 6087128.
 ACCESSION ARI02867
 VERSION ARI02867.1 GI:12814455
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 309)
 AUTHORS Nolan, L.K., Horne, S.M.
 TITLE DNA encoding an avian E. coli 1ss
 JOURNAL Patent: US 6087128-A 6 11-JUL-2000;
 FEATURES Location/Qualifiers
 source 1. 309
 /organism="unknown"
 BASE COUNT 97 a 69 c 65 g 78 t
 ORIGIN
 Query Match 81.6%; Score 252; DB 6; Length 309;
 Best Local Similarity 88.6%; Pred. No. 7.6e-54;
 Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
 OY 1 atgcaggaataaagaatgaataaataatgttatttctgcgcgtctgcgaatgttataca 60
 DB 1 ATGCAGGATTAATTAAGATGAATAAATGTTATTTCTGCCGCTCGCAATGCTTATTACA 60
 OY 61 ggaatggtcccaacaacgcttactgttgaacaacaacgcagcagtaacacaaaggaa 120
 DB 61 GGATGTGCTCAACAAACGTTTACTGTGGAACAAACCAACCACTAACCACAAAGGAA 120
 OY 121 accatcacatcatattcttcgttcggaattggaacaagaagaactgttgtagcc 180
 DB 121 ACCATCACATCATTTCTTCCTCCCAATGAGC-AGAGAAAAGCTTGATGAGCC 180
 OY 181 aaatttg-tggcgggtgcagaaaatgtgttaaacagaaactgcgaacttgtaaa 240
 DB 181 AAAATTGTTGGCGGTGAGAAAATGTTTAAACAGAACTGACCAAACTTGCTAAA 240
 OY 241 ggaatggtcccaacaacgcttactgttgaacaacaacgcagcagtaacacaaaggaa 300
 DB 241 GGATGTGCTCAACAAACGTTTACTGTGGAACAAACCAACCACTAACCACAAAGGAA 300
 OY 301 tcaacaata 308
 DB 301 TCACAAATA 308
 RESULT 12
 ARI29411
 LOCUS ARI29411 309 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 6 from patent US 6187321.
 ACCESSION ARI29411
 VERSION ARI29411.1 GI:14117308
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 309)
 AUTHORS Nolan, L.K., Horne, S.M. and Robinson, M.
 TITLE Avian E. coli 1ss polypeptide
 JOURNAL Patent: US 6187321-A 6 13-FEB-2001;
 FEATURES Location/Qualifiers
 source 1. 309
 /organism="unknown"
 BASE COUNT 97 a 69 c 65 g 78 t
 ORIGIN
 Query Match 81.6%; Score 252; DB 6; Length 309;
 Best Local Similarity 88.6%; Pred. No. 7.6e-54;
 Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 atcgagataataaagatgaagaaatgtatcttcgctgcgtctggcaatgctattaca 60
 Db 1 ATCGGAGATTAACACCACTGAAAAAATGCTACTGCTACTGCGCTGCGCTGTTATTACA 60
 QY 61 ggaatgtctcaacaacagcttctactgttggaaacacacagcagcgtatacaccagaagaa 120
 Db 61 GGATGTGCTCAACAGACGCTTACTGTTCAAAACAAACCGCGCAGCGAGTACACCAAGAA 120
 QY 121 accatcatcatcattcttcgttcggaattggacagaagaacagctgtatgacagc 180
 Db 121 ACCATCACCCATCATTTCTTCTGCTTGTGGAATGGGAGAAAGAACTGTGATGACAGCC 180
 QY 181 aaatttggcgggtgcagaaatgtgttaaaacagaactcagcaaacattcgttaaa 240
 Db 181 AAAATTTGTGGCGCGGCAAAAATGTGTAAACAGAAACCCAGCAACATTCGTAAT 240
 QY 241 ggaatgtcgggtttatctacttttggcactatactcgcgtggaagcccggtatattgc 300
 Db 241 GGATGTGCTCGGTTTATTACTTAGGCATTATACCTCGCTGGAAGCGCGTGTATTGCG 300
 QY 301 tcacata 308
 Db 301 TCACATA 308

RESULT 13

BLANLON
 LOCUS Bacteriophage lambda bor gene. 326 bp DNA Linear PHG 04-MAR-1994
 DEFINITION X55792
 ACCESSION X55792.1 GI:288763
 VERSION X55792.1
 KEYWORDS envelope protein.
 SOURCE bacteriophage lambda.
 ORGANISM bacteriophage lambda.
 Viruses: dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae; lambda phage group.
 1 (bases 1 to 326)
 Barondess, J.J. and Beckwith, J.
 A bacterial virulence determinant encoded by lysogenic coliphage lambda
 Nature 346 (6287), 871-874 (1990)

REFERENCE 1 (bases 1 to 326)
 AUTHORS Barondess, J.J. and Beckwith, J.
 TITLE A bacterial virulence determinant encoded by lysogenic coliphage lambda
 JOURNAL Nature 346 (6287), 871-874 (1990)
 MEDLINE 90363299
 FEATURES
 SOURCE Location/Qualifiers
 1..326
 /organism="bacteriophage lambda"
 /db_xref="taxon:10710"
 24..317
 /gene="bor"
 24..317
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 /codon_start=1
 /transl_table=11
 /protein_id="CAA39317.1"
 /db_xref="GI:288764"
 /translation="MKMLATLALITGCAOQFTVONKPAVAKETITTHFFVS
 GIGOKTVDAKICGAEVNYKTETQTFVNGLIGFTLGIYPLEARYVCSQ"

CDS
 gene
 24..317
 /gene="bor"
 24..317
 /gene="bor"
 /codon_start=1
 /transl_table=11
 /protein_id="CAA39317.1"
 /db_xref="GI:288764"
 /translation="MKMLATLALITGCAOQFTVONKPAVAKETITTHFFVS
 GIGOKTVDAKICGAEVNYKTETQTFVNGLIGFTLGIYPLEARYVCSQ"

BASE COUNT 104 a 72 c 69 g 81 t
 ORIGIN

Query Match 81.6%; Score 252; DB 7; Length 326;
 Best Local Similarity 88.6%; Pred. No. 7.6e-54;
 Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 atcgagataataaagatgaagaaatgtatcttcgctgcgtctggcaatgctattaca 60
 Db 1 ATCGGAGATTAACACCACTGAAAAAATGCTACTGCTACTGCGCTGCGCTGTTATTACA 68
 QY 61 ggaatgtctcaacaacagcttctactgttggaaacacacagcagcgtatacaccagaagaa 120
 Db 61 GGATGTGCTCAACAGACGCTTACTGTTCAAAACAAACCGCGCAGCGAGTACACCAAGAA 128
 QY 121 accatcatcatcattcttcgttcggaattggacagaagaacagctgtatgacagc 180
 Db 121 ACCATCACCCATCATTTCTTCTGCTTGTGGAATGGGAGAAAGAACTGTGATGACAGCC 188
 QY 181 aaatttggcgggtgcagaaatgtgttaaaacagaactcagcaaacattcgttaaa 240
 Db 181 AAAATTTGTGGCGCGGCAAAAATGTGTAAACAGAAACCCAGCAACATTCGTAAT 248
 QY 241 ggaatgtcgggtttatctacttttggcactatactcgcgtggaagcccggtatattgc 300
 Db 241 GGATGTGCTCGGTTTATTACTTAGGCATTATACCTCGCTGGAAGCGCGTGTATTGCG 308
 QY 301 tcacata 308
 Db 301 TCACATA 316

QY 121 accatcatcatcattcttcgttcggaattggacagaagaacagctgtatgacagc 180
 Db 129 ACCATCACCCATCATTTCTTCTGCTTGTGGAATGGGAGAAAGAACTGTGATGACAGCC 188
 QY 181 aaatttggcgggtgcagaaatgtgttaaaacagaactcagcaaacattcgttaaa 240
 Db 189 AAAATTTGTGGCGCGGCAAAAATGTGTAAACAGAAACCCAGCAACATTCGTAAT 248
 QY 241 ggaatgtcgggtttatctacttttggcactatactcgcgtggaagcccggtatattgc 300
 Db 249 GGATGTGCTCGGTTTATTACTTAGGCATTATACCTCGCTGGAAGCGCGTGTATTGCG 308
 QY 301 tcacata 308
 Db 309 TCACATA 316

RESULT 14

LOCUS 002453 9170 bp DNA Linear SYN 29-MAR-1996
 DEFINITION Cloning vector lambda EMBL3, right arm.
 ACCESSION 002453
 VERSION 002453.1 GI:413819
 KEYWORDS
 SOURCE Cloning vector lambda EMBL3.
 ORGANISM Cloning vector lambda EMBL3.
 Cloning vector lambda EMBL3.
 Artificial sequence: vectors.
 1 (bases 1 to 9170)
 Kitz, P.A.
 Clontech Vectors on Disc version 1.3
 Kitz, P.A.
 Unpublished
 2 (bases 1 to 9170)
 Frischauf, A.M., Lehrach, H., Poustka, A. and Murray, N.
 Lambda replacement vectors carrying polylinker sequences
 J. Mol. Biol. 170 (4), 827-842 (1983)
 MEDLINE 84064856
 REFERENCE 3 (bases 1 to 9170)
 Kitz, P.A.
 Direct Submission
 Submitted (07-OCT-1993) Paul A. Kitz, Clontech Laboratories, Inc.,
 1020 East Meadow Circle, Palo Alto, CA 94303, USA
 This sequence has been compiled from information in the sequence
 databases, published literature and other sources. If you suspect
 there is an error in this sequence, please contact Clontech's
 Technical Service Department at (415) 424-8222 or (800) 662-2666,
 extension 3 or e-mail TECH@CLONTECH.COM.

COMMENT
 JOURNAL
 TITLE
 AUTHORS
 MEDLINE
 REFERENCE
 1020 East Meadow Circle, Palo Alto, CA 94303, USA
 This sequence has been compiled from information in the sequence
 databases, published literature and other sources. If you suspect
 there is an error in this sequence, please contact Clontech's
 Technical Service Department at (415) 424-8222 or (800) 662-2666,
 extension 3 or e-mail TECH@CLONTECH.COM.

FEATURES
 SOURCE Location/Qualifiers
 1..9170
 /organism="Cloning vector lambda EMBL3"
 /db_xref="taxon:31783"
 2534 a 1996 c 2251 g 2389 t

BASE COUNT 2534 a 1996 c 2251 g 2389 t
 ORIGIN

Query Match 81.6%; Score 252; DB 12; Length 9170;
 Best Local Similarity 88.6%; Pred. No. 6.4e-54;
 Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 atcgagataataaagatgaagaaatgtatcttcgctgcgtctggcaatgctattaca 60
 Db 7435 ATCGGAGATTAACACCACTGAAAAAATGCTACTGCTACTGCGCTGCGCTGTTATTACA 7376
 QY 61 ggaatgtctcaacaacagcttctactgttggaaacacacagcagcgtatacaccagaagaa 120
 Db 7375 GGATGTGCTCAACAGACGCTTACTGTTCAAAACAAACCGCGCAGCGAGTACACCAAGAA 7316
 QY 121 accatcatcatcattcttcgttcggaattggacagaagaacagctgtatgacagc 180
 Db 7315 ACCATCACCCATCATTTCTTCTGCTTGTGGAATGGGAGAAAGAACTGTGATGACAGCC 7256
 QY 181 aaatttggcgggtgcagaaatgtgttaaaacagaactcagcaaacattcgttaaa 240
 Db 181 AAAATTTGTGGCGCGGCAAAAATGTGTAAACAGAAACCCAGCAACATTCGTAAT 248

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 11:04:54 ; Search time 2538.62 Seconds
(without alignments)
2009.694 Million cell updates/sec

Title: US-09-738-599-21

Perfect score: 378

Sequence: 1 cctgaagctctgtccaggg.....ggagctcatcgcgaattcc 378

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues 27472414

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST :
1: em_estb1:
2: em_estb2:
3: em_estb3:
4: em_estb4:
5: em_estb5:
6: em_estb6:
7: em_estb7:
8: em_estb8:
9: em_estb9:
10: em_estb10:
11: em_estb11:
12: em_estb12:
13: em_estb13:
14: em_estb14:
15: em_estb15:
16: em_estb16:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	232	61.4	332	9	AM619529 7594 MARC
2	187.2	49.5	731	9	AV398499 AV398499
3	143.8	38.0	240	9	AM659631 97104 MAR
4	139.8	37.0	785	9	A1547008 PN2.1-13-
5	123.8	32.8	223	10	C22108 M1YA
6	120.6	31.9	160	10	BG895793 359430 MA
7	119	31.5	160	10	BG835172 353618 MA
8	109.6	29.0	162	10	B1338974 363710 MA
9	109.4	28.9	336	10	BE518841 M22A1STM
10	89.4	23.7	178	10	BE521841 EST35576
11	65.8	17.4	802	9	A1546999 PN2.1-12-
12	63.2	16.7	594	10	BE493915 WHE1276_B
13	45.4	12.0	299	9	AA547917 MB3D6V2GO
14	45.2	12.0	560	12	B84811 RPCI11-28F7
15	45.2	12.0	634	12	AO309897 CTBT-EI-
16	42.8	11.3	532	12	AO544521 CTBT-EI-
17	38.8	10.3	733	12	A2131766 OSUNB011

18	38.8	10.3	914	12	A2539756
19	38.6	10.2	426	9	AV532310
20	38.6	10.2	599	9	AV537481
21	38.4	10.2	520	12	A2927608
22	38	10.1	514	10	BM168198
23	37.4	9.9	183	12	B88032
24	37.4	9.9	524	12	A2525395
25	37.4	9.8	488	12	AG024048
26	37.2	9.8	942	12	CNS02631
27	37.2	9.8	404	10	BI514353
28	37	9.8	458	10	BI510802
29	37	9.8	559	10	BI510865
30	36.8	9.7	478	9	AM288591
31	36.8	9.7	582	12	AQ629690
32	36.8	9.7	681	12	A2522631
33	36.8	9.7	681	10	BE658070
34	36.4	9.6	733	10	BF680474
35	36.2	9.6	500	9	A0086381
36	36	9.5	617	12	A2856405
37	36	9.5	713	12	BH029375
38	36	9.5	1101	12	CNS01610
39	35.8	9.5	494	10	B1745078
40	35.8	9.5	496	9	AA842275
41	35.6	9.4	885	12	CNS013ET
42	35.4	9.4	771	9	AL516158
43	35.4	9.4	1101	12	CNS05RM7
44	35.2	9.3	392	10	BM258478
45	35.2	9.3	468	9	AV618307

ALIGNMENTS

RESULT 1
LOCUS AM619529/c 332 bp mRNA linear EST 24-MAR-2000
DEFINITION 7594 MARC PBE Sus scrofa CDNA 5', mRNA sequence.
ACCESSION AM619529
VERSION AM619529.1 GI:7325713
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE Smith,T.P.L., Fahrenkrug,S.C., Rohrer,G.A., Slommen,F.A., Rexroad
,C.E. and Keefe,J.W.
Mapping of expressed sequence tags from a porcine early embryonic
CDNA library
Anim. Genet. 32 (2), 66-72 (2001)

JOURNAL
MEDLINE
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.980904.e. Vector identified by cross-match with the -m1nscore 18
and -m1match 12 options.
PCR Primers
FORWARD: GGAACAGCTATGACCATG
BACKWARD: GTAAACGAGCGGACGT
Seq primer: AATTAACCTCTACCAAGG.
Location/Qualifiers
1. 332
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC PBE"
/tissue_type="Dry 12 whole embryos"
/lab_host="X10LR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Library made from pool of embryos in spherical and

FEATURES
source

ORIGIN

BASE COUNT ORIGIN	70 a	51 c	52 g	6 / e
----------------------	------	------	------	-------

Query Match	38.08;	Score 143.8;	DB 9;	Length 240;
Best Local Similarity	90.18;	Pred. No. 5.6e-30;		

	Matches	154;	Conservative	0;	Mismatches	17;	Indels	0;	Gaps	0;
QY	176	tttcgggaattcggacagaagaactgttcatgctgcaccaaatttctgctgcgtgcagaaa	235							
Db	240	TTTTCTGGAAATTGGCGCAGAGAAAACTGTCTGATGACGCCAAATTTGTGGCGCGCGA	181							
QY	236	atgtgttcaaaaacagaactcagcaaacatttgttaatggatctgcgttttacactt	295							
Db	180	ATGTGTGTTAAACAGAAACCCACCAAAATCTGTAATGAGATTGCTGGTTTATTACTT	121							
QY	236	ttcgcatctatactcgcgtcgtgaagcccggtatattgtctcaccaatnattggc	346							
Db	120	TAGGATTATTACTCTCCCTGGAGCGCCTGTGTATTGTCTCCCAATTAATTGC	70							

RESULT	4
A1547008/c	
LOCUS	
DEFINITION	765 bp mRNA
ACCESSION	U09496
VERSION	1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	TITLE
AUTHORS	JOURNAL
	MEDLINE
	COMMENT
Ucarali, V.C., Metacala, C., Churruarín, C., Canals, J., Verticoulakis, E., Eutelsio, L.M., Mammalia, J., Eutheria, J., Primates, C., Catarrhini, J., Homiidae, J., Homo, I. (bases 1 to 785)	Prostate cancer expression profiling by cDNA sequencing analysis
Huang, G.M., Ng, W.L., Farkas, J., He, L., Liang, H.A., Gordon, D., Yu, J. and Hood, L.	Genomics 59 (2), 178-186 (1999)
Contact: Guyang Matthew Huang	99339982

Deloy Hood
 University of Washington
 Department of Molecular Biotechnology, Box 357730, University of
 Washington, Seattle, WA 98195
 Tel: 5106280100
 Fax: 5106280108
 Email: huanggm@yahoo.com.

Location/Qualifiers	Source
1. .785	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone_id="mynorm"	
/note="Organ: Prostate; Vector: pBluescript; Directional cDNA library was constructed using Lambda Zap II kit (Stratagene). mRNA was extracted from a frozen normal prostate tissue (Mayo Clinic)."	
153 a 128 c 147 g 229 t 128 others	
BASE COUNT	
ORIGIN	

Query Match	37.0%	Score 139, 8:	DB, 9:	Length 785;
Best Local Similarity	78.0%	Pred. No. 9.5e-29;		
Matches 199; Conservative	0;	Mismatches 52;	Indels 4;	Gaps 3;

Oy	42	taaaagatgaaaaaaatgtcatcttctgcgcgcctctgcgaatgctattcaagagatgyc	101
Db	255	TAATACACTCNCATTAANGCNAATTGGTACCGGNCGCCCGCTTANTACAGGAAGTTC	196

QY --tcacacaacgtttctctgttcgaac-aacacgcagcagcagcaccacaagaagaaac-a 157
102 |||||
Db CACCAACAGAGCTTACTGCTCAAAACAAACCGCGCAGCAGTAGCACCACCAAGCAACCA 136
195

QY	158	135	Db
toactcatcattcttcggttcgsgaattcgsgcaagsgaaaaactgttgatcagccaaa	217		
tcaccatcatttcttcggttcggaattggcgagaaagaaaactgtcgcgatcgacgccaaa	76		

Oy 218 ttctgtgcgcgtgcagaaatctgttctaaaccagaactcagcaacattcgtaaatgatt 277
 Db 75 ttgttgccgcgcgcagcaaaattgttttaaacagaaaccacagcaaacatttcgttaanangatt 16

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QY      278  tgcctcggtttatca 292
          |||||
Db      15  TGCTCGGTNTATTA 1

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RESULT	5
C22108	
LOCUS	
DEFINITION	C22108 Myagawa-wase satsuma mandarin orange (M.Omura) Citrus
ACCESSION	unshiu cDNA clone pCMFR1719.66, mRNA sequence.
	223 bp mRNA linear EST 29-JUN-1999

VERSION	C22108.1	GI:1669108
KEYWORDS	EST.	
SOURCE	Citrus unshiu.	
ORGANISM	Citrus unshiu	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 223)	Hisada,S., Akihama,T., Endo,T., Moriuchi,T. and Omura,M	Expressed sequence tags of Citrus fruit during rapid cell development phase	J. Amer. Soc. Hort. Sci. 122, 808-812 (1997)	Contact: Mitsuo Omura

Department of Citriculture
National Institute of Fruit Tree Science, Okitsu
Okitsu, Shimaizu, Shizuoka 424-02, Japan
Tel: +81-543-69-2111
Tel: +81-543-69-2115
Fax: +81-543-69-2115
Email: cm9330@ok.affrc.go.jp
PROJECT - Citrus genome Analysis.

```

SOURCE
LOCATIONS/VARIETALS
1. .223
/organism="Citrus unshiu"
/strain="Miyagawa-wase satsuma mandarin"
/db_xref="taxon:51188"
/clone="pckFR1719.66"
/clone_id="Miyagawa-wase satsuma mandarin orange (M.Omura)"
/tissue_type="juice sac and pulp segment"
/dev_stage="rapid developing stage"
BASE COUNT 70 a 50 c 52 g 51 t
ORIGIN

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Query Match	32.8%	Score 123.8	DB 10	Length 223
Best Local Similarity	80.5%	Pred. NO. 2.3e24		
Matches 157	Conservative	0	Mismatches 37	Indels 1
				Gaps 1

QY 39 ggaataacagagatgaataaaatgttattttctgcgcctctggcagaatgctattatccagatg 98
Db 13 GAATAAACCCATGAAAAAATGCTACTCGCTACTGTGGCCCTGCTATTATACAGGATG 72

QY | tggccaaacaaggtttcctglttggaaaacaaaccgcagcagtcacacccaagaagcaatc 158
| |||||
Db | 73 TGTCTCAACAGAGGTTTACTGTCTCAAACCAACCGGCACAGTAGCACCACAAGGAACCAT 132

0y caccacacatctcttcgttttcgggaattggacacagagaaacatgcttgatgcagccaatat 218
 159 |
 133 caccatcatattcttcgttttcgggaattgggc - agagaaacctgttgccagccaaaatt 191
 Db

Qy	219	ttgtgcggtgcaga	233
Db	192	TTGGGCCGAGGAAA	206

RESULT 6
EG895793/C

LOCUS B68957.1 160 bp mRNA linear EST 05-JUN-2001
DEFINITION 359430 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION B68957.1
VERSION B68957.1 GI:14306034
KEYWORDS EST.

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

plg.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
1 (bases 1 to 160)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACATCGACGAG
Plate: 123 row: L column: 23
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. 160
/organism="Sus scrofa"
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/clone_id="MARC 1Pig"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 46 a 37 c 31 g 46 t
ORIGIN

Query Match 31.9%; Score 120.6; DB 10; Length 160;
Best Local Similarity 93.3%; Pred. No. 1.7e-23;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 212 ccaaaattgtgctgaggaataatgtttaaacaagaactcgaacattcgtaa 271
DB 160 CCAAAATTGTGCTGCGCGCGAGAAAATGTGTTAAACAGAACCCGCAACATTGCTAA 101

OY 272 atggaattgctcggtttatcactcttggacatcctacccgctggaagccgggtatatt 331
DB 100 ATGGAATTGCTCGGTTTATTACTTTAGCATTTATATCTCCGCGAGAACCGCGTGTATT 41

OY 332 gctcacaaatagttgc 346
DB 40 GCTCACAAATATATTGC 26

RESULT 7
LOCUS BG835172 160 bp mRNA linear EST 25-MAY-2001
DEFINITION BG835172 353618 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BG835172
VERSION BG835172.1 GI:14201080
KEYWORDS EST.
SOURCE
ORGANISM
PIG.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
1 (bases 1 to 160)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine

JOURNAL
COMMENT
FEATURES

Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACATCGACGAG
Plate: 116 row: L column: 23
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. 160
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_id="MARC 1Pig"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 47 a 37 c 31 g 45 t
ORIGIN

Query Match 31.5%; Score 119; DB 10; Length 160;
Best Local Similarity 92.6%; Pred. No. 4.9e-23;
Matches 125; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 212 ccaaaattgtgctgaggaataatgtttaaacaagaactcgaacattcgtaa 271
DB 160 CCAAAATTGTGCTGCGCGCGAGAAAATGTGTTAAACAGAACCCGCAACATTGCTAA 101

OY 272 atggaattgctcggtttatcactcttggacatcctacccgctggaagccgggtatatt 331
DB 100 ATGGAATTGCTCGGTTTATTACTTTAGCATTTATATCTCCGCGAGAACCGCGTGTATT 41

OY 332 gctcacaaatagttgc 346
DB 40 GCTCACAAATATATTGC 26

RESULT 8
LOCUS B1338974 162 bp mRNA linear EST 30-JUL-2001
DEFINITION B1338974 363710 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
ACCESSION B1338974
VERSION B1338974.1 GI:15032257
KEYWORDS EST.
SOURCE
ORGANISM
PIG.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
1 (bases 1 to 162)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.

BASE COUNT	46 a	34 c	40 g	58 t
ORIGIN				
Query Match	23.7%	Score 89.4	DB 10	Length 178
Best Local Similarity	82.9%	Pred. No. 1.1e-14		
Matches 102	Conservative 0	Mismatches 21	Indels 0	Gaps 0
OY	33	catgcagataataagatgaaaaaatgttattcttcgcgcctcttgcaatgcttattac	92	
Db	123	CATCGGGAATTAACACCAATGAAAAAATCTACTGCTACTCGCGGCGCTGCTATTAC	64	
OY	93	aggatgtctcaacaacagttactctgttggaacaaacgcagcagtaaacacaaagga	152	
Db	63	AGGATGCTCTCAACAGAGCTTACTGTTCAAAACAAACGGCAGCAGTAGACCAAAAGGA	4	
-OY	153	aac 155		
Db	3	AAC 1		
RESULT 11				
LOCUS	AI546999	802 bp	mRNA	linear
DEFINITION	PN.1.12.G12.r mynorm Homo sapiens CDNA 5', mRNA sequence.			
ACCESSION	AI546999			
VERSION	AI546999.1	GI:4464487		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 802)			
AUTHORS	Huang,G.M., Ng,W.L., Parkas,J., He,L., Liang,H.A., Gordon,D., Yu,J. and Hood,L.			
TITLE	Prostate cancer expression profiling by cDNA sequencing analysis			
JOURNAL	Genomics 59 (2), 178-186 (1999)			
MEDLINE	99339982			
COMMENT	Contact: Guyang Matthew Huang Leroy Hood University of Washington Department of Molecular Biotechnology, Box 357730, University of Washington, Seattle, WA 98195 Tel: 5106280100 Fax: 5106280108 Email: huanggm@yahoo.com.			
FEATURES	Location/Qualifiers			
source	1..802			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone_1lb="mynorm"			
	/note="Organ: Prostate; Vector: pBluescript; Directional			
	cdna library was constructed using lambda ZP II kit			
	(Stratagene). mRNA was extracted from a frozen normal			
	prostate tissue (Mayo Clinic). 125 others			
BASE COUNT	179 a	152 c	163 g	183 t
ORIGIN				
Query Match	17.4%	Score 65.8	DB 9	Length 802
Best Local Similarity	88.6%	Pred. No. 6.2e-08		
Matches 70	Conservative 0	Mismatches 9	Indels 0	Gaps 0
OY	151	gaacacatcacataattcttcgttcggtggaatgcgacaagagaanaactgttgatga	210	
Db	1	GAACACCATCCACCAATCTTCTGCGTTCGGAATGGCGCAAGAAAACACTGTCGATGCA	60	
OY	211	gccaaattgttgcgagtg	229	
Db	61	GCCAAATTTGTGGCGCG	79	
RESULT 12				

FEATURES	BE493915	LOCUS	594 bp	MRNA	linear	EST 02-AUG-2000
DEFINITION	WHE1276_B06.C1225 Secale cereale	another cDNA library	Secale cereale			
ACCESSION	BE493915					
VERSION	BE493915.1	GI:9660508				
KEYWORDS	EST.					
SOURCE	ye.					
ORGANISM	Secale cereale					
REFERENCE	Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae					
AUTHORS	1 (bases 1 to 594)					
	Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton					
	R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R.,					
	Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and Tong, J.C.					
TITLE	The structure and function of the expressed portion of the wheat					
	genomes - Another cDNA library from rye					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Olin Anderson					
	US Department of Agriculture, Agriculture Research Service, Pacific					
	West Area, Western Regional Research Center					
	800 Buchanan Street, Albany, CA 94710, USA					
	Tel: 5105959773					
	Fax: 5105959518					
	Email: oanderson@pw.usda.gov					
	Sequence has been trimmed to remove vector sequence and low					
	quality sequence with phred score less than 20					
	Seq primer: Stragatene SK primer.					
	Location/Qualifiers					

SOURCE	Location/Qualifiers
	1..594
	/organism="Secale cereale"
	/cultivar="Blanco"
	/db_xref="taxon:4550"
	/clone_1id="WBH1276_306.C12"
	/clone_1lb="Secale cereale anther cDNA library"
	/tissue_type="Anther"
	/dev_stage="Adult plant before anthesis"
	/lab_host="E. coli SOLR"
	/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
	Site:1: EcoRI; Site:2: XhoI; Plants were grown in the
	greenhouse. Anthers were harvested and pooled from early
	meiosis to late meiosis. The tissue, total RNA, and
	poly(A) RNA were prepared (Butler, Ross and Gustafson at
	University of Missouri, Columbia). A cDNA library was
	made, and the cDNA clones were in vivo excised to give
	phagescript phagmids in the T7 Close lab (Choi, Close,
	Renton) at the University of California, Riverside.
	Plasmid DNA preparations and DNA sequencing were performed
	in the OD Anderson lab (all other authors)."
BASE COUNT	136 a 150 c 142 g 166 t
ORIGIN	
Query Match	16.7%; Score 63.2; DB 10; Length 594;
Best Local Similarity	89.5%; Pred No.3.2e-07;
Matches 68; Conservative	0; Mismatches 8; Indels 0; Gaps 0;
Dy 271	aatgatactgcgtttacatttcacatttgccatcattaccgcgcggaaagcccggtatatc 330
Dd 17	AAGGATTCCTCGCTTTATTACTTATGACATTATATCTCCGCTGGAAAGCGGTGTGTAT 76
Dy 331	tgtcacataagtgc 346
Dd 77	TGCTCACAAATAATTGC 92
RESULT 13	
AA547917/c	
LOCUS	299 bp mRNA linear EST 22-SEP-1997
DEFINITION	M83D6VZ0505 Brugia malayi day 6 post-infection third stage larvae
	SANB6MLM-BHL3d6 Brugia malayi cDNA clone 3D6VZ0505 5', mRNA
	sequence.

Claim 1; SEQ ID No 29743; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridization probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94554 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
XX
50 Sequence 1023 BP: 267 A; 267 C; 267 G; 217 T; 0 other;

Query Match	Score	DB	Length
Best Local Similarity	81.8%	Pred. No. 0.098	
Matches	45	Conservative	0
		Mismatches	10
		Indels	0
		Gaps	0

RESULT 15
AAA26702

AC AAA26702;

DT 23-JUN-2000 (first entry)

Candida albicans polynucleotide sequence #40.

KM *Candida albicans* infection; growth; survival; medicament; AIDS
KM vulvovaginitis; immunocompromised patient; treat; ss.

OS *Candida albicans*.
 XX
 PN EP982401-A2.
 XX
 PD 01-MAR-2000.
 XX
 PF 23-DEC-1998; 98EP-0310694.
 XX
 PR 14-AUG-1998; 98GB-0017796.
 XX
 PA (JANC) JANSSEN PHARM NV.
 XX
 PI Contreras RH, Nelissen B, De Backer MD, Luyten WHML, Viaene JE;
 PI Loghe MG;
 XX
 DR WPI; 2000-258614/23.
 XX

Claim 1; Page 78; 133pp; English.

CC This sequence represents a polynucleotide sequence encoding a polypeptide
CC that is critical for the survival and growth of *Candida albicans*. The
CC *C. albicans* nucleic acid molecules of the invention may be used as probes
CC and primers for detecting homologous nucleic acid molecule sequences.
CC The polypeptides and nucleic acid molecules and compounds identified as
CC selectively modulating the expression of the polypeptides, may be used as
CC medicaments or for the preparation of a medicament to treat *C. albicans*
CC associated diseases, especially in AIDS patients and to treat
CC vulvovaginitis in otherwise healthy females. The use of the polypeptides
CC and polynucleotide sequences to treat *C. albicans* associated diseases has
CC fewer side effects and less toxicity than previously used methods such as
CC the use of amphotericin. This method is therefore especially suitable for
CC immunocompromised patients, such as AIDS patients.

SQ Sequence 1685 BP; 650 A; 281 C; 250 G; 504 T; 0 other;

Query Match	9.68;	Score 36.2;	DB 21;	Length 1685;
Best Local Similarity	59.08;	Pred. No. 0.81;		
Matches 62;	Conservative 0;	Mismatches 43;	Indels 0;	Gaps 0;

OY 142 acacccaagaacccatcatctctcttcgttcgttggaattggacaagaagaact 201
 Db 1334 acacaccgcgaacccacccatttaattcatatcgcgcagatgatggaagaagtgaatt 1399
 OY 202 gtctgatgcagccaattgtgtgcggtgcgcagaanaatgctgtttaa 246
 Db 1394 agtcatgatgatttatctctgatgaagaagatgaagaattgaa 1438

Search completed: July 23, 2002, 13:51:26
Job time: 5377 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 12:19:59 ; Search time 99.46 Seconds
(Without alignments)
933.536 Million cell updates/sec

Title: US-09-738-599-21

Perfect score: 378
Sequence: 1 ctggaagttctgtccagg.....ggagctcattcgtcattc 378

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/1na/6A.COMB.seq: *
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/1na/PTCUS.COMB.seq: *
6: /cgn2_6/ptodata/2/1na/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	378	100.0	378	3	US-09-023-221A-21 Sequence 21, Appl
2	378	100.0	378	4	US-09-282-352A-21 Sequence 21, Appl
3	339.8	89.9	760	3	US-09-023-221A-1 Sequence 1, Appl
4	339.8	89.9	760	4	US-09-282-352A-1 Sequence 1, Appl
5	309	81.7	309	3	US-09-023-221A-22 Sequence 22, Appl
6	309	81.7	309	4	US-09-282-352A-22 Sequence 22, Appl
7	273.2	72.3	309	3	US-09-023-221A-5 Sequence 5, Appl
8	273.2	72.3	309	4	US-09-282-352A-5 Sequence 5, Appl
9	256.4	67.8	11933	4	US-09-470-618-13 Sequence 13, Appl
10	256.4	67.8	11933	4	US-09-364-862-13 Sequence 13, Appl
11	252	66.7	309	3	US-09-023-221A-6 Sequence 6, Appl
12	252	66.7	309	4	US-09-282-352A-6 Sequence 6, Appl
13	34.2	9.0	1519	4	US-09-002-361-4 Sequence 1, Appl
14	33.6	8.9	1817	2	US-08-743-637B-1 Sequence 1, Appl
15	33.6	8.9	1817	2	US-08-526-840B-1 Sequence 1, Appl
16	32.8	8.7	4380	1	US-07-582-945-1 Sequence 1, Appl
17	32.8	8.7	4380	2	US-08-453-141-1 Sequence 1, Appl
18	32.8	8.7	4380	3	US-08-293-314-1 Sequence 1, Appl
19	32.4	8.6	1925	2	US-08-553-436A-1 Sequence 1, Appl
20	32.2	8.5	408	4	US-09-328-111-169 Sequence 169, App
21	32.2	8.5	1690	1	US-08-276-452A-24 Sequence 24, Appl
22	32.2	8.5	1690	2	US-08-798-744-24 Sequence 24, Appl
23	31.2	8.3	90050	4	US-09-245-041-5 Sequence 5, Appl
24	30.6	8.1	1504	2	US-08-878-989-10 Sequence 10, Appl
25	30.6	8.1	1504	4	US-09-272-796-10 Sequence 10, Appl
26	30.6	8.1	1576	2	US-09-197-378-1 Sequence 1, Appl
27	30.2	8.0	2089	1	US-08-552-142A-1 Sequence 1, Appl

28	30.2	8.0	2089	1	US-08-910-973-1 Sequence 1, Appl
29	30.2	8.0	2089	5	PCT-US95-05741-1 Sequence 11, Appl
30	30	7.9	34	3	US-09-023-221A-11 Sequence 11, Appl
31	30	7.9	34	4	US-09-282-352A-11 Sequence 15, Appl
32	29.8	7.9	2431	3	US-08-714-918-15 Sequence 15, Appl
33	29.8	7.9	2431	4	US-09-265-315-15 Sequence 15, Appl
34	29.8	7.9	2431	4	US-09-265-315-15 Sequence 15, Appl
35	29.8	7.9	2431	4	US-09-265-315-15 Sequence 15, Appl
36	29.8	7.9	2943	2	US-08-788-892-1 Sequence 1, Appl
37	29.6	7.8	2525	3	US-08-714-918-84 Sequence 84, Appl
38	29.6	7.8	2525	4	US-09-265-315-84 Sequence 84, Appl
39	29.6	7.8	2525	4	US-09-265-315-84 Sequence 84, Appl
40	29.6	7.8	2525	4	US-09-265-315-84 Sequence 84, Appl
41	29.6	7.8	3825	3	US-08-904-263A-3 Sequence 3, Appl
42	29.4	7.8	237	3	US-08-904-263A-5 Sequence 5, Appl
43	29.4	7.8	421	4	US-08-976-259-92 Sequence 92, Appl
44	29.4	7.8	846	2	US-08-743-637B-189 Sequence 189, App
45	29.2	7.7	595	4	US-09-385-982-25 Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-023-221A-21
Sequence 21, Application US/09023221A
Patent No. 6087128
GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
INVENTOR: HORNE, SHELLEY M.
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MEETING, RAASCH & GERHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023, 221A
FILING DATE: 12-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-023-221A-21

Query Match: 100.0%; Score 378; DB 3; Length 378;
Best Local Similarity: 100.0%; Pred. No. 3.2e-112;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ctggaagttctgtccaggccctggatcattcaggaataaagatgaataatg 60
1 ctggaagttctgtccaggccctggatcattcaggaataaagatgaataatg 60
1 ctggaagttctgtccaggccctggatcattcaggaataaagatgaataatg 60

QY 61 ttatttcgcgcctcgtgcaatgcttattacagagatgctcaacaacgittactgtt 120
|||||
Db 61 TATTITTCGCCGCTTGCCAACTGCTTATTACAGATGTCCTCAACAAACGTTACTGTT 120
QY 121 ggaacaaacgcagcagtaacacccaagaagaaacatactcaatcattcttcglttcg 180
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Db 121 GGAACAAACCCAGACAGCAATACACCAAGAAACCATCATCATCTTCCTTCGTTTCG 180
QY 181 ggaattggacaagagaacactgttgatgacccaataatttggcggtgcagaataatgtt 240
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Db 181 GGAATTGGACAAGAGAAACTGTGTATGACGCAAAATTTGGCGGTGCAGAAATVGT 240
QY 241 gtttaaacagaacactcagaacacattcgttaaatgattgctcggttttacttcgttcg 300
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Db 241 GTTAAACAGAAACTCAGCAAACTTCGTAATGATGCTCGTTTATCATTTCGTC 300
QY 301 atctatactcgcctggaagcccggtatattgctcacaaatagttgccatgatatggg 360
|||||
Db 301 ATCTATACCTCCGCTGGAAGCCCGGGATATGTCTCACAATAGTTGCCCATATATGGGG 360
QY 361 agctcatctgcgaattcc 378
|||||
Db 361 AGCTCATCTGCGAATTC 378

RESULT 2

US-09-282-352A-21
Sequence 21, Application US/09282352A
Patent No. 6187321

GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
APPLICANT: ROBINSON, MICHAEL
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUEITING, RAASCH & GERHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282.352A
FILING DATE: 31-MAR-1999

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/023.221
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00010102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-282-352A-21

Query Match 100.0%; Score 378; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 3.2e-112;

Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctggaagttcttcttcgaagggcccttggatctcagatcaataatgaaaaaag 60
|||||
Db 1 CTGGAAGTTCTCTTCAGGGGCCCTGGATCTCATGCAAGATAATGAATGAAAAAATG 60
QY 61 ttatttcgcgcctcgtgcaatgcttattacagagatgctcaacaacgittactgtt 120
|||||
Db 61 TATTITTCGCCGCTTGCCAACTGCTTATTACAGATGTCCTCAACAAACGTTACTGTT 120
QY 121 ggaacaaacgcagcagtaacacccaagaagaaacatactcaatcattcttcglttcg 180
|||||
Db 121 GGAACAAACCCAGACAGCAATACACCAAGAAACCATCATCATCTTCCTTCGTTTCG 180
QY 181 ggaattggacaagagaacactgttgatgacccaataatttggcggtgcagaataatgtt 240
|||||
Db 181 GGAATTGGACAAGAGAAACTGTGTATGACGCAAAATTTGGCGGTGCAGAAATVGT 240
QY 241 gtttaaacagaacactcagaacacattcgttaaatgattgctcggttttacttcgttcg 300
|||||
Db 241 GTTAAACAGAAACTCAGCAAACTTCGTAATGATGCTCGTTTATCATTTCGTC 300
QY 301 atctatactcgcctggaagcccggtatattgctcacaaatagttgccatgatatggg 360
|||||
Db 301 ATCTATACCTCCGCTGGAAGCCCGGGATATGTCTCACAATAGTTGCCCATATATGGGG 360
QY 361 agctcatctgcgaattcc 378
|||||
Db 361 AGCTCATCTGCGAATTC 378

RESULT 3

US-09-023-221A-1
Sequence 1, Application US/09023221A
Patent No. 6087128

GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
APPLICANT: ROBINSON, MICHAEL
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUEITING, RAASCH & GERHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.221A
FILING DATE: 12-FEB-1998

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-023-221A-1

Query Match 81.7%; Score 309; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 4.2e-90;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 34 atgcagataaataagatgataaaatgtatattctgcgcctctggcaatgcttata 93
DB 1 ATGCAGATAAATAAGATGATAAAATGTAATTTCTGCGCTGTGGCAATGCTTATTACA 60
OY 94 ggaatgtctcaacaacgcttactgttggaaacacgacagcagtaacccaaggaa 153
DB 61 GGATGTGCTCAACAAACGTTTACTGTGGAAACCAACGACGACTAACACCAAGGAA 120
OY 154 accatcactcatcattcttctgttcgggaattggacaagaagaacatctgtacagcc 213
DB 121 ACCATCCTCATCATCTTCTCTGTTGGAAATGGACAGAAACCTTTATGACAGCC 180
OY 214 aaattgtgctgctgacagaataatgtttaaacaagaactcagcaaacatctgtaaat 273
DB 181 AAAATTGTGGCGGTGACAGAAATGTTTAAACAGAACTCAGCAAACTCGTAAT 240
OY 274 ggaatgtcgtgttataacttttggcactatactcgcgtggaagccgggtatattgc 333
DB 241 GGATGTGCTGCTGTTTATCATCTTGTGGCACTATCTCCGCTGGAAGCCCGGTATATTGC 300
OY 334 tcacaatag 342
DB 301 TCACAAATAG 309
```

RESULT 6

US-09-282-352A-22
Sequence 22, Application US/09282352A

Patent No. 6187321
GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
APPLICANT: ROBINSON, MICHAEL
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,352A
FILING DATE: 31-MAR-1999
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 09/023,221
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255,00010102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-282-352A-22

Query Match 81.7%; Score 309; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 4.2e-90;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 34 atgcagataaataagatgataaaatgtatattctgcgcctctggcaatgcttata 93
DB 1 ATGCAGATAAATAAGATGATAAAATGTAATTTCTGCGCTGTGGCAATGCTTATTACA 60
OY 94 ggaatgtctcaacaacgcttactgttggaaacacgacagcagtaacccaaggaa 153
DB 61 GGATGTGCTCAACAAACGTTTACTGTGGAAACCAACGACGACTAACACCAAGGAA 120
OY 154 accatcactcatcattcttctgttcgggaattggacaagaagaacatctgtacagcc 213
DB 121 ACCATCCTCATCATCTTCTCTGTTGGAAATGGACAGAAACCTTTATGACAGCC 180
OY 214 aaattgtgctgctgacagaataatgtttaaacaagaactcagcaaacatctgtaaat 273
DB 181 AAAATTGTGGCGGTGACAGAAATGTTTAAACAGAACTCAGCAAACTCGTAAT 240
OY 274 ggaatgtcgtgttataacttttggcactatactcgcgtggaagccgggtatattgc 333
DB 241 GGATGTGCTGCTGTTTATCATCTTGTGGCACTATCTCCGCTGGAAGCCCGGTATATTGC 300
OY 334 tcacaatag 342
DB 301 TCACAAATAG 309
```

RESULT 7

US-09-023-221A-5
Sequence 5, Application US/09023221A

Patent No. 6087128
GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,221A
FILING DATE: 12-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255,00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-023-221A-5

Query Match 72.3%; Score 273.2; DB 3; Length 309;
Best Local Similarity 96.8%; Pred. No. 1.3e-78;
Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

QY 34 atgcagataataagaatgaaataatgtatttctgcgcgtctgcaatgtattaca 93
1 ATGCAGATTAATTAAGTAAAGAAAAATGTTATTTCTGCCCCCTCGCAATGCTATTACA 60
DB 94 ggaatgtctcaacaacggttactgttggaaacaacacagcagtaacacaaaggaa 153
61 GGATGTGCTCAACAACGTTTACTGTTGGAACAAACCGACAGTAACACCAAGAA 120
QY 154 aacatcaactatcattcttccttctgggaattggacaagaagaactgttgcagcc 213
121 ACCATCACTCATATTTCTTCTGTTCCCAATTGGAC-AGAGAAACTGTGATGCAGCC 179
DB 214 aaatttg-tggcggtcagagaataatgtttaaacaagaactcagcaaatcgttaa 272
180 AAATTTGTTGGCGGTGAGAAAAATGTTTAAACAGAAACACAGAAACATTGCTAAA 239
QY 273 tggattgctcggttttatacactttggcatctatactcgcgtggaagccgggtatattg 332
240 TGCATTCGCCGCTTTTATCACTTTTGGCATCTATACCTCCGCGGAAACCGGTATATTTG 299
DB 333 ctcaaatag 342
DB 300 CTCACAATAG 309

RESULT 8

US-09-282-352A-5
Sequence 5, Application US/09282352A
Patent No. 6187321

GENERAL INFORMATION:
APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHEILEY M.
APPLICANT: ROBINSON, MICHAEL
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEETING, RAASCH & GERHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,352A
FILING DATE: 31-MAR-1999
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 09/023,221
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255,00010102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-282-352A-5

Query Match 72.3%; Score 273.2; DB 4; Length 309;
Best Local Similarity 96.8%; Pred. No. 1.3e-78;
Matches 300; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

QY 34 atgcagataataagaatgaaataatgtatttctgcgcgtctgcaatgtattaca 93
1 ATGCAGATTAATTAAGTAAAGAAAAATGTTATTTCTGCCCCCTCGCAATGCTATTACA 60
DB 94 ggaatgtctcaacaacggttactgttggaaacaacacagcagtaacacaaaggaa 153
61 GGATGTGCTCAACAACGTTTACTGTTGGAACAAACCGACAGTAACACCAAGAA 120
QY 154 aacatcaactatcattcttccttctgggaattggacaagaagaactgttgcagcc 213
121 ACCATCACTCATATTTCTTCTGTTCCCAATTGGAC-AGAGAAACTGTGATGCAGCC 179
DB 214 aaatttg-tggcggtcagagaataatgtttaaacaagaactcagcaaatcgttaa 272
180 AAATTTGTTGGCGGTGAGAAAAATGTTTAAACAGAAACACAGAAACATTGCTAAA 239
QY 273 tggattgctcggttttatacactttggcatctatactcgcgtggaagccgggtatattg 332
240 TGCATTCGCCGCTTTTATCACTTTTGGCATCTATACCTCCGCGGAAACCGGTATATTTG 299
DB 333 ctcaaatag 342
DB 300 CTCACAATAG 309

RESULT 9

US-09-470-618-13
Sequence 13, Application US/09470618
Patent No. 6200560

GENERAL INFORMATION:
APPLICANT: Colosi, Linda B.
APPLICANT: Colosi, Peter C.
TITLE OF INVENTION: Adeno-associated Vectors for Expression of Factor VIII
FILE REFERENCE: Avigen-04082
CURRENT APPLICATION NUMBER: US/09/470,618
CURRENT FILING DATE: 1999-12-22
EARLIER APPLICATION NUMBER: 09/364,862
EARLIER FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/104,994
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 11933
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-470-618-13

Query Match 67.8%; Score 256.4; DB 4; Length 11933;
Best Local Similarity 88.5%; Pred. No. 1.7e-72;
Matches 278; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 33 catgcagataataagaatgaaataatgtatttctgcgcgtctgcaatgtattac 92
9294 catgcagataataacacagaaataatgtactcgtactcgtcgtcgtcgtattac 9353
DB 93 aggaatgtctcaacaacggttactgttggaaacaacacagcagtaacacaaaggaa 152
9354 aggaatgtctcaacaacggttactcgttcaaaacaacacagcagtaacacaaaggaa 9413
QY 153 aacatcaactatcattcttccttctgggaattggacaagaagaactgttgcagc 212

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Db 9414 aaccatccaccatcattcttcgttctgcatctgagagaagaacatgctgacgcagc 9473
Oy 213 caaatctgtgctgagagaagaatgtgttaaacagaaactcgcgaacatctgttaa 272
Db 9474 caaatctgtgctgagagaagaatgtgttaaacagaaactcgcgaacatctgttaa 9533
Oy 273 tggattgctggtttatcacttttgcatctatactcgcgtggaagccggtatattg 332
Db 9534 tggattgctggtttatcacttttgcatctatactcgcgtggaagccggtatattg 9593
Oy 333 ctcaacaatgtgc 346
Db 9594 ctcaacaatgtgc 9607

```

```

: SUIT 10
: US-09-364-862-13
: Sequence 13, Application US/09364862
: Patent No. 6223349
: GENERAL INFORMATION:
: APPLICANT: Couto, Linda B.
: TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII
: TITLE OF INVENTION: BY TARGET
: FILE REFERENCE: AVIGEN-03743
: CURRENT APPLICATION NUMBER: US/09/364,862
: CURRENT FILING DATE: 1999-07-30
: EARLIER APPLICATION NUMBER: 60/125,974
: EARLIER FILING DATE: 1999-03-24
: EARLIER APPLICATION NUMBER: 60/104,994
: EARLIER FILING DATE: 1998-10-20
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 13
: LENGTH: 11933
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: US-09-364-862-13

```

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Query Match 67.8%; Score 256.4; DB 4; Length 11933;
Best Local Similarity 88.5%; Pred. No. 1,7e-72;
Matches 278; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```

```

Oy 33 catcagagataataagatgaaaaaatttcttctgcgcctctgcaatgtattac 92
Db 9294 catcagagataataagatgaaaaaatttcttctgcgcctctgcaatgtattac 9353
Oy 93 aggtgtgctcaacaagaagtttactgttgaaacaacgcagacgaatgaacccaaga 152
Db 9354 aggtgtgctcaacaagaagtttactgttgaaacaacgcagacgaatgaacccaaga 9413
Oy 153 aaccatcctcatcattcttcttctggttgcgaattggaacaagaagaactgtgtgacgc 212
Db 9414 aaccatcctcatcattcttcttctggttgcgaattggaacaagaagaactgtgtgacgc 9473
Oy 213 caaatctgtgctgagagaagaatgtgttaaacagaaactcgcgaacatctgttaa 272
Db 9474 caaatctgtgctgagagaagaatgtgttaaacagaaactcgcgaacatctgttaa 9533
Oy 273 tggattgctggtttatcacttttgcatctatactcgcgtggaagccggtatattg 332
Db 9534 tggattgctggtttatcacttttgcatctatactcgcgtggaagccggtatattg 9593
Oy 333 ctcaacaatgtgc 346
Db 9594 ctcaacaatgtgc 9607

```

```

RESULT 11
US-09-023-221A-6
: Sequence 6, Application US/09023221A
: Patent No. 6087128
: GENERAL INFORMATION:
: APPLICANT: NOLAN, LISA K.
: APPLICANT: HORNE, SHELLEY M.
: TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MEETING, RAASCH & GEBHARDT P.A.
: STREET: 119 NORTH FOURTH STREET, SUITE 203
: CITY: MINNEAPOLIS
: STATE: MN
: COUNTRY: U.S.A.
: ZIP: 55401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/023,221A
: FILING DATE: 12-FEB-1998
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: SANDBERG MS., VICTORIA A.
: REGISTRATION NUMBER: 41,287
: REFERENCE/DOCKET NUMBER: 255.00010101
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (612) 305-1226
: TELEFAX: (612) 305-1228
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 309 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-09-023-221A-6

```

```

Query Match 66.7%; Score 252; DB 3; Length 309;
Best Local Similarity 88.6%; Pred. No. 8.4e-72;
Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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```

Oy 34 atgcagataataagataaaaaaatttcttctgcgcctctgcaatgtattac 93
Db 1 ATCGGGAATACACCATGAAAAAATGCTACTGCTACTGCGCTGCGCTGCTATTAC 60
Oy 94 ggaatgtctcaacaagaagtttactgttgaaacaacgcagacgaatgaacccaaga 153
Db 61 GGATGTGCTCAACAGACGTTACTGTCAAAACAAACCGCGCAGTAGACCAACAAAG 120
Oy 154 accatcctcatcattcttcttctggttgcgaattggaacaagaagaactgtgtgacgc 213
Db 121 ACCATCACCACCAATCTTCTCTCTGGAATGGGCAAGAAACGTCATCACCAC 180
Oy 214 aaattctgtgctgagagaagaatgtgttaaacagaaactcgcgaacatctgttaa 273
Db 181 AAAATTGTGCGCGCGCGCAAAAATGTGTAAACAGAAACCCACCAAACTTCTAAT 240
Oy 274 ggaatgtcgtttatcacttttgcatctatactcgcgtggaagccggtatattg 333
Db 241 GGATGTGCTGAGTTTATTACTTAGGCAATTTACTCCGCTGGAAGCGGTGTATTGC 300
Oy 334 tcacaata 341
Db 301 TCACAATA 308

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```

RESULT 12
US-09-282-352A-6

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	Query Match	66.7%	Score 252:	DB 4:	Length 309;	
	Best Local Similarity	88.6%:	Pred. No. 8.4e-72:			
	Matches 273:	Conservative	0:	Mismatches 35:	Indels	0; Gaps
Oy	34 atgcgataataagatgaataaaaaatgtattcttcgcgcgtctgycgaatgtattaca	93				
Dd	1 ATCGGAGTAATACACCATGAATAAAATGGCTACTCGGTACTGCCTGCCCTGGTTATTACA	60				
Oy	94 ggaagtgtctcaacaaagcgtttactctgttggaaaacaacgcagcgccgttaaccacaaggaa	153				
Dd	61 GGATGTGCTCAACACACGCTTACTGTTAAAAAACAACGGCAGCGATGACACCACCAAAGGA	120				
Oy	154 accactactcatcatcttcgttcgttcgggaatcttgacaagaagaaaacgttgtacgcc	213				
Dd	121 ACCATCACCCATTCATTTCTCTGCTTCCTGGAATTTGGCGAGAATAAACTGTGCATCGACGC	180				
Oy	214 aaaatctgtgcgcgtgcagaaaaatgltgtttaaacagaaaactcagcaaacatctgtaaat	273				
Dd	181 AAAATTGTGGCGGGCGAGAAAATGTTGTTAAAAAGAAACCCACCAAAACATTCGTAAT	240				
Oy	274 ggattgctcggttttatcatacttttggcatctatactccgctctggaagcccgggtatatgic	333				
Dd	241 GGATTGCTCGGCTTTTATTACTTTAGGCATTTTACTCCGCTGGAAAGCGGTGTGATTGTC	300				
Oy	334 tcaacata 341					
Dd	301 TCACATA 308					

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Query Match          9.0%; Score 34.2; DB 4; Length 1519;
Best Local Similarity 67.6%; Pred. No. 0.15; 23; Indels    0; Gaps    0;
Matches   48; Conservative      0; Mismatches              0;

QY       186  tgcacagagaacaactcgtgatgcagccaaattctgtcgctgcagaanaatcgtttaa 245
           ||| ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db        992  TGGCAAAAGAGAATACGATCGAATAAACAAAGATTGTGGCCATACAGAAAATAGCTTCG 1051

QY       246  aaacgaaacac 256
           || |||||| |

Db        1052 AAAAGAAAAATC 1062

RESULT  14
US-08-743-637B-1
; Sequence 1, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; PROBS AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
```

;; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
;; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
;; NUMBER OF SEQUENCES: 273
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: QUARLES & BRADY
;; STREET: 411 EAST WISCONSIN AVENUE
;; CITY: MILWAUKEE
;; STATE: WISCONSIN
;; COUNTRY: USA
;; ZIP: 53202-4497
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/743,637B
;; FILING DATE: 04-NOV-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/526,840
;; FILING DATE: 11-SEP-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BAKER, Jean C.
;; REGISTRATION NUMBER: 35,433
;; REFERENCE/DOCKET NUMBER: 850586, 90012
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (414) 277-5000
;; TELEFAX: (414) 277-5591
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1817 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; ORGANISM: Enterococcus faecalis
;; US-08-743-637B-1

Query Match 8.9%; Score 33.6; DB 2; Length 1817;
Best Local Similarity 51.3%; Pred. No. 0.25;
Matches 78; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

OY 160 accatcattcttcgttcggaattgacagagaacacgttgatgcagccaaatt 219
DB 1211 ACCTATGCTTCCTTGAATGATGAGTGGTCATGAATGACATGCTGTGACGGAACAT 1270

OY 220 tctgagcggtgcagaaatgttgttaaacagaaactcagcaaacattcgtaaatgattg 279
DB 1271 ACTGCGGCTTAAATATTAGACAAATCAGTGCCTTGAATGAATCTTATCTGATTG 1330

OY 280 ctgcgtttatcacctttggcatctactcc 311
DB 1331 ATGGGTATATATTTCGGGTGATCTAATCC 1362

RESULT 15
US-08-526-840B-1
; Sequence 1, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: QUARLES & BRADY

;; STREET: 411 East Wisconsin Avenue
;; CITY: Milwaukee
;; STATE: Wisconsin
;; COUNTRY: USA
;; ZIP: 53202-4497
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/526,840B
;; FILING DATE: 11-SEP-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/304,732
;; FILING DATE: 12-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BAKER, Jean C.
;; REGISTRATION NUMBER: 35,433
;; REFERENCE/DOCKET NUMBER: 850586, 90012
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (414) 277-5000
;; TELEFAX: (414) 277-5591
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1817 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; ORGANISM: Enterococcus faecalis
;; US-08-526-840B-1

Query Match 8.9%; Score 33.6; DB 3; Length 1817;
Best Local Similarity 51.3%; Pred. No. 0.25;
Matches 78; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

OY 160 accatcattcttcgttcggaattgacagagaacacgttgatgcagccaaatt 219
DB 1211 ACCTATGCTTCCTTGAATGATGAGTGGTCATGAATGACATGCTGTGACGGAACAT 1270

OY 220 tctgagcggtgcagaaatgttgttaaacagaaactcagcaaacattcgtaaatgattg 279
DB 1271 ACTGCGGCTTAAATATTAGACAAATCAGTGCCTTGAATGAATCTTATCTGATTG 1330

OY 280 ctgcgtttatcacctttggcatctactcc 311
DB 1331 ATGGGTATATATTTCGGGTGATCTAATCC 1362

Search completed: July 23, 2002, 13:45:07
Job time: 5108 sec

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